

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gatanaga, Tetsuya  
Granger, Gale A.
- (ii) TITLE OF INVENTION: Factors Altering Tumor Necrosis  
Factor Receptor Releasing Enzyme Activity.
- (iii) NUMBER OF SEQUENCES: 154
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: BOZICEVIC, FIELD, & FRANCIS, LLP  
(B) STREET: 200 MIDDLEFIELD ROAD, #200  
(C) CITY: Menlo Park  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94025
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: Windows  
(D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 09/700,354  
(B) FILING DATE: 13-NOV-2000  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 09/081,385  
(B) FILING DATE: 14-MAY-1998  
  
(A) APPLICATION NUMBER: PCT/US99/10793  
(B) FILING DATE: 14-MAY-1999
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Francis, Carol L.  
(B) REGISTRATION NUMBER: 36,513  
(C) REFERENCE/DOCKET NUMBER: IRVN-007CIP2
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 650-327-3400  
(B) TELEFAX: 650-327-3231  
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4047 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

09700354-1.1.3.0

AAGCTTTTTG	CTTTCCTTCC	CCGGGAAAAGG	CCGGGGGCCAG	AGACCCGCAC	TCGGACCAGG	60
CGGGGGCTGC	GGGGCCAGAG	TGGGCTGGGG	AGGGCTGGGA	GGGCGTCTGG	GGCCGGCTCC	120
TCCAGGCTGG	GGGCCGCCAG	CTCCGGGAAG	GCAGTCTTGG	CCTGCGGATG	GGGCCGCGCG	180
TGGGGCCCCG	CGGGGCGGCC	TCGGGAGGCG	TCCAGGCTGC	GGGAGCGGGA	GGAGCGGCCG	240
TGCGGGCGCC	AGCGCCGTGG	GTGGAGGTCG	CCGTCCCTCC	TGAGGGGCAG	CCAGTGCGTT	300
TGGGACCCGG	GAGCAGAGCC	CGCGCTCCC	CAGCGGCCTC	CCCGGGGGTC	TCACCGGGTC	360
ACCCGAGAGC	GGAGGCCCCG	GCTCCGCAGA	AACCCGGGGC	GGCCGCGGGG	AAGCAGCGCC	420
CTCAGGCGTC	GGAGGAGCCC	CCAGAAGGAC	CTCGCGCCTT	CCCGCCGGGC	TCCGACCGCC	480
TGGGTTCGGT	GCGGGACGGC	CCAGGCCGCC	AGGACCCCA	AGCGCAGCTC	AGTCTGCGGG	540
GCACGACCCA	GAGGCCAGCA	GCAGAGGACG	GGGCCGGGGC	CGGGAGAGGG	CGGGGAGGGC	600
GCTCCTGGGA	GGTCAAGGCC	AGGGCTAGAC	TTTCAGGGTC	ATGGCCTGGC	CCCTCATCCC	660
CAGGGAGGTG	AGGGGGCTCT	GTGAGCAGAG	GGGGCCCCGG	TGGAGAAGGC	GCTGCTAGCC	720
AGGGGCGGGG	CAGGAGCCCA	GGTGGGGACT	TAAGGGTGGC	TGAAGGGACC	CTCAGGCTGC	780
AGGGATAGGG	AGGGAAGCTA	GGGGTGTGGC	TTGGGGAGGT	GCTGGGGGAC	CGCGGGCGCC	840
CTTTATTCTG	AAGCCGAATG	TGCTGCCGGA	GTCCCCAGTG	ACCTAGAAAT	CCATTTC AAG	900
ATTTTCAGGA	GTTTCAGGTG	GAGACAAAGG	CCAGGCCCAG	GTGAAAATGT	GGCAGTGACA	960
GAGTATGGGG	TGAGAACCAC	GGAGAGAGGA	AGTCCCCGAG	GCGGATGATG	GGACAGAGAG	1020
CGGGGACCAG	AATTTTTTAA	AACGCATCTG	AGATGCGTTT	GGCAGACTCA	TAGTTGTTTT	1080
CCTTTCACGG	AGAAAGTG TG	GGCAGAAGCC	AGCTCTAAAG	CCCAGGCTGC	CCAGCCTGCA	1140
CTGGCAGAGC	TGACGGAAGG	CCAGGGCAGA	GCCTTCCCTC	CCTGTACACAG	ACATGAGCCC	1200
TGGAGATCTG	GAATGAGGCA	GATGTGCCCA	GGGAAAGCTG	ATCCGCCCCG	ACCCAGGGCC	1260
CCCCGGGTGC	CCCTTTGAGC	GTGGAATCGT	TGCCAGGTCA	TGGCTCCCTG	CTATCGAACA	1320
CCGGACACGG	GTCGTGTGCT	GCACCTGGCA	GTTGCAGGAC	CGACACCCAC	AATGCCTTAA	1380
GAGGTGATGA	CTGCCTTCCA	GGGGCCTGGC	TGGCTGACAC	TTTGCATGGC	TCCTGGAGAA	1440
GAGGGATTGA	GTGGAGTCCA	CGGGTCATGG	CCACGTCTTG	GGTGCTGCCT	CTGAGGCAGG	1500
GCCCGGCTGG	GGTGAGAAGG	GGCTGGAGAC	AGGTTCTCTG	CAGTTCAGCC	TCTAACCGGT	1560
GGTCTTCATG	CCTAGGAACC	CACCTGGGGC	TTATGAAACT	GCAGGTGGCT	GAGTCCCTGC	1620
CATGGGGTCT	CTCCTTCAGG	AGGTCTGGGT	GGGGCCGGAG	ACTGTACCCC	ACAAAGGGTC	1680
CCAGGTGAGG	CGGATGTGGC	CTGGCGCTGT	GTGGCTCTGG	ACCTAGTCCT	TGGGCTTGGG	1740
CTGGCGCCCA	GGGCCTGGGC	TTGAGACAGC	TGTGACGCAG	GCAAGCCATT	TACCCCGTTT	1800
GTGGGGACAT	TACATCTTCC	TAGCTTGGA	CACACAGGCA	GCCAGGGTTG	TTATCCACAT	1860
TCCTCTCCA	TGTTCTTCTC	TTGAGAACTT	TTACCAGGTA	TGTCAGGAGC	TGGGCTCCAC	1920
CAGGGAGACT	CAAGTGGA	GCCCTCATCC	TTGTCTCCA	GGAGACAGGA	AAACCTATGG	1980
TTACAATTCC	AGGGACAAGA	GCGATGCATG	TGAGGTGTGG	CAAATCTCAC	TGTTCAACTG	2040
GAGAAATCAG	AGACAGCTTC	CTGGAGGCAG	TGACACCTGG	ACAGGCTTCT	CCACAGGAGG	2100
AAGCGAGTGA	GAGAAGCCAA	CTGGGATGGA	CCCATCATGT	AGGGGGAACA	GTGCGCGCAG	2160
AACCAACAAC	CACCCCCACC	CTAGGCCCAG	AGCTCACGGA	GAGAGCTGGG	CCTCTCGGGG	2220
TGACTACATA	GTTCCCTGCT	GGATCTTAGG	TCTTGTCTTT	GGGCAGCTCT	GCTGAGACCT	2280
CTATGCCTGT	TCCAGGCTGC	ACCAAGGTTT	TGTGACTATT	GGTCTGGGGT	TGTTTTGCAG	2340
CAACTGAAGT	GTTCTGTTGT	AAAACAGGCA	CTTGATTTGC	TGGAAGGAAT	GCTGTTTGT	2400
CTTGCTGCGA	CAAACATTGA	GCAGCATTTA	GTGGGCGGTT	TATATCTTGT	GGAGTAATGG	2460
GTGTTTTTGA	AGTCTGTCTT	GGGTACTGCA	CATTAAAAGG	AATATCATTT	TCTGAAACAT	2520
TGCTATTTTC	CACACCAGAA	ATCATATCCT	CTTGCTGGTC	CATGTCTGAA	GACCTTACAC	2580
GAGAAAGTCT	TAATGTAAGT	TTAGTAGAGT	CCTTGAGATG	AGAACTAATT	ATATCATACA	2640
TTGCCGCTTT	CTCACTCTGC	TCTTTTTTCA	CCTTGCCTAA	TTTCATTTTC	TTCTGCTTCT	2700
TTTGTTTTCT	TTCTGGAGAA	TCTAGCAAGA	TATCTGGTGG	AACATCTCGA	GGTGATGAAC	2760
AAGGTAGAGA	CTGAGATTGT	AGGATTAAAG	GTGGTCTTGA	GCCTTTAGGA	GTTCCCTTCAC	2820
TTCCAGCAGG	GGAGCATACT	GGCTGTGGAG	ATCTCAAGGG	AAAAGATGCA	GCATTCTCTCA	2880
TTGTTGAAGA	ATCTCCATCG	TCACTACTTA	GCCTGTGCAC	CATGTGTAGG	TAGTCCTCAC	2940
TTGAACCATG	TCTAGGATTA	TCAGCATGAT	GATTAGCTGA	ATTGCCAGAC	AACGGACCAG	3000

AAACTTTATT	ATCATGTATG	TTTCTCAAAC	CACCTGCAAC	AATGGGACTT	GATACCGATG	3060
CTTGTTGCAT	CTGTGGATGT	GTTGTGTAAC	TTGAAGGATG	GGAATATGGC	ATGTATCCTG	3120
CAGGGCTTTG	TGGGGCGTAT	GGACTAGGCA	CTGGGCTATT	TTGCTGTGGC	ATAAATCTGT	3180
TCCCAGAGCT	TGTCTGTGGT	GGCACAAACC	GGCTGGAGGG	GCTATGTGAG	ATAGTGGTTT	3240
GTTGATAATT	GGAAGATGCA	GGACTACTGT	GCATGGAATT	CTGAGAAAGT	TTATACTGAG	3300
ACATCATCAT	TCCACTTTGT	ACATATCTGT	TCTGCATGCT	TTTCTCCCTG	AAAACATTAG	3360
GACTCCTTGC	CAGGACGGCC	TGCAACAAGA	CTGGTATGTC	ACCTTCTGGG	TCATCACTGC	3420
CAAGGTTATC	TTTCAACTCT	ATGTGATCTG	TTGATACCTG	GTTGAGGCTA	TGGACAAGCT	3480
GTGAAACCAA	ATTGTCATCC	CTACAAGCCA	AAAGGCAGTT	CACCTCTTCT	GCTATTCTGT	3540
CATTAAAGAG	AAGGCTCTTT	GTAGTTGTAG	CAGGTAAAGG	AGATGGAAGA	GGCAGCTGGT	3600
TCAGGAGGTC	TGTGAGACTA	GCAATCCCCG	CAAGAGTAGT	AATGGGGACA	TGGGGCATAT	3660
CCCCATT CAT	CCTGAATTTT	TGGAATGGTG	TTGCCATAAA	AAGTACTTAG	TTCAGGTGCC	3720
AGCTGTCATT	ACTTCCCATT	TCCCAAACAC	TGGGCGAATC	GGCGTCTGAA	TCCAAGGGGA	3780
GGCCGAGGCC	GCTGTGGCGA	GAGACTATAA	TCCGGGCCGG	GAGGGGGGGC	GGCTACGGCT	3840
CCTCTTCCGT	CTCCTCAGTG	CGGGGAACAT	GTAAGGCCGG	GGGGAGACCA	GCCGAGAAGA	3900
CAAATCGTTG	CTTCTTCTTC	CTCCTCCTCC	TCCTTCTCCC	ACATAGAAAC	ACTCACAAAC	3960
ACCCGACCAC	GGGCCCGAGC	TACCGGGGGG	GCATCGCCGC	GGGCCCGGGA	ACCAATTCTC	4020
CTGTCGGCGG	GGGCGTCCTT	TGGATCC				4047

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGATCCAAAG	GTCAAACCTCC	CCACCTGGCA	CTGTCCCCGG	AGCGGGTCGC	GCCCCGGCCGG	60
CGCGCGGCCG	GGCGCTTGGC	GCCAGAAGCG	AGAGCCCCTC	GGGGCTCGCC	CCCCCGCCTC	120
ACCGGGTCAG	TGAAAAAACG	ATCAGAGTAG	TGGTATTTCA	CCGCGCGCCC	GCAGGGCCGG	180
CGGACCCCGC	CCCGGGCCCC	TCGCGGGGAC	ACCGGGGGGG	CGCCGGGGGC	CTCCCACTTA	240
TTCTACACCT	CTCATGTCTC	TTCACCGTGC	CAGACTAGAG	TCAAGCTCAA	CAGGGTCTTC	300
TTTCCCCGCT	GATTCCGCCA	AGCCCGTTCC	CTTGGCTGTG	GTTTCGCTGG	ATAGTAGGTA	360
GGGACAGTGG	GAATCTCGTT	CATCCATTCA	TGCGCGTCAC	TAATTAGATG	ACGAGGCATT	420
TGGCTACCTT	AAGAGAGTCA	TAGTTACTCC	CGCCGTTTAC	CCGCGCTTCA	TTGAATTTCT	480
TCACTTTGAC	ATTCAGAGCA	CTGGGCAGAA	ATCACATCGC	GTCAACACCC	GCCGCGGGCC	540
TTCGCGATGC	TTTGTTTTAA	TTAAACAGTC	GGATTCCCCT	GGTCCGCACC	AGTTCCTAAGT	600
CGGCTGCTAG	GCGCCGGCCG	AAGCGAGGCG	CCGCGCGGAA	CCGCGGCCCC	CGGGGCGGAC	660
CCGCGGGGGG	GACCGGGCCG	CGGCCCTCC	GCCGCCTGCC	GCCGCGCCG	CCGCCGCGCG	720
CCGAAGAAGA	AGGGGGAAA					739

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAAGAGTGGC	GGCCGCAGCA	GGCCCCCGG	GTGCCCGGGC	CCCCCTCGAG	GGGGACAGTG	60
CCCCCGCCGC	GGGGGCCCCG	CGGCGGGCCG	CCGCCGGCCC	CTGCCGCCCC	GACCTTCTC	120
CCCCCGCCGC	CGCCCCACG	CGGCGTCCC	CCGGGGAGGG	GGGAGGACGG	GGAGCGGGG	180
AGAGAGAGAG	AGAGAGAGGG	CGCGGGGTGG	CTCGTGCCGA	ATTCAAAAAG	CTT	233

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGATCCAAAG	AATTCGGCAC	GAGGTAGTCA	CGGCTCTTGT	CATTGTTGTA	CTTGACGTTG	60
AGGCTGGTGA	GCTTGAAAAA	GTCGATGCGC	AGCGTGACAGC	AGGCGTTGTA	GATGTTCTGC	120
CCGTCCAGCG	ACAGCTTGGC	GTGCTGGGCG	CTCACGGGGT	CCGCATACTG	CAGCAGGGCC	180
TGGAACGGT	TGTTCTTGGT	GAAGGTGATG	ATCTTCAACA	CTGTGCCGAA	CTTGGAGAAA	240
ATCTGGTGCA	GCACATCCAG	GGTCACAGGG	TAGAAGAGGT	TCTCCACGAT	GATCCTGAGC	300
ACGGGGCTCT	GCCCGGCCAT	CGCCATCCCT	GCATCCACGG	CCGCCGCCGA	GGCAGCCAAG	360
GCCAGGTTCC	CCGACTGGAC	CGAGTTCACC	GCCTGCAGGG	CCGCCTGGGC	CCGCGCCTGG	420
TTGGGAGAGC	TGTCGGTCTT	CAGCTCCTTG	TGGTTGGAGA	ACTGGATGTA	GATGGGCTGG	480
CCGCGCAGCA	CAGGGGTCAC	CGAGGTGTAG	TAGTTCACCA	TGGTATTGGC	AGCCTCCTCC	540
GTGTTCACTCT	CGATGAAGGC	CTGGTTTTTC	CCCTTCAGCA	TCAGGAGGTT	GGTGACCTTC	600
CCAAAGGGCA	GCCCCAGGGA	GATGACTTCC	CCCTCCGTGA	CGTCGATGGG	GAGCTTCCGG	660
ATGTGGATCA	CTCTAGAGGG	GACGCCTGCA	CTTCGGCTGT	CACCTTTGAA	CTTCTTGCTG	720
TCATTTCCGT	TTGCTGCAGA	AGCCGAGTTG	CTGCTCATGA	TAAACGGTCC	GTTAGTGACA	780
CAAGTAGAGA	AAAGCTCGTC	AGATCCCCGC	TTTGTACCAA	CGGCTATATC	TGGGACAATG	840
CCGTCCATGG	CACACAGAGC	AGACCCGCGG	GGGACGGAGT	GGAGGCGCCG	GAATCCTGGA	900
GCTAGAGCTG	CAGATTGAGT	TGCTGCGTGA	GACGAAGCGC	AAGTATGAGA	GTGTCTTGCA	960
GCTGGGCCGG	GCACTGACAG	CCCACCTCTA	CAGCCTGCTG	CAGACCCAGC	ATGCACTGGG	1020
TGATGCCTTT	GCTGACCTCA	GCCAGAAGTC	CCCAGAGCTT	CAGGAGGAAT	TTGGCTACAA	1080
TGCAGAGACA	CAGAAACTAC	TATGCAAGAA	TGGGGAAACG	CTGCTAGGAG	CCGTGAACTT	1140
CTTTGTCTCT	AGCATCAACA	CATTGGTCAC	CAAGACCATG	GAAGACACGC	TCATGACTGT	1200
GAAACAGTAT	GAGGCTGCCA	GGCTGGAATA	TGATGCCTAC	CGAACAGACT	TAGAGGAGCT	1260
GAGTCTAGGC	CCCCGGGATG	CAGGGACACG	TGGTCGACTT	GAGAGTGCCC	AGGCCACTTT	1320
CCAGGCCCCAT	CGGGACAAGT	ATGAGAAGCT	GCGGGGAGAT	GTGGCCATCA	AGCTCAAGTT	1380
CCTGGAAGAA	AACAAGATCA	AGGTGATGCA	CAAGCAGCTG	CTGCTCTTCC	ACAATGCTGT	1440
GTCCGCCTAC	TTTGCTGGGA	ACCAGAAACA	GCTGGAGCAG	ACCCTGCAGC	AGTTCAACAT	1500
CAAGCTGCGG	CCTCCAGGAG	CTGAGAAACC	CTCCTGGCTA	GAGGAGCAGT	GAGCTGCTCC	1560
CAGCCCAACT	TGGCTATCAA	GAAAGACATT	GGGAAGGGCA	GCCCCAGGGT	GTGGGAGATT	1620
GGACATGGTA	CATCCTTTGT	CATTGCCCCT	CTGGCTTGGG	CTCCTTTTTT	TGGCTGGGGC	1680
CTGACACCAG	TTTTGCCAC	ATTGCTATGG	TGGGAAGAGG	GCCTGGAGGC	CCAGAAGTTG	1740
CTGCCCTGTC	TATCTTCCTG	GCCACAGGGC	TTCATTCCCA	GATCTTTTCC	TTCCACTTCA	1800
CAGCCAACGG	CTATGACAAA	ACCACTCCCT	GGCCAATGGC	ATCACTCTTC	AGGCTGGGGT	1860
GTGCTCCCTG	ACCAATGACA	GAGCCTGAAA	ATGCCCTGTC	AGCCAATGGC	AGCTCTTCTC	1920
GGACTCCCCCT	GGGCCAATGA	TGTTGCGTCT	AATACCTTTT	GTCTCTCCTC	TATGCGTGCC	1980
CATTGCAGAG	AAGGGGACTG	GGACCAAAGG	GGTGGGGATA	ATGGGGAGCC	CCATTGCTGG	2040
CCTTGCACTCT	GAATAGGCCT	ACCCTCACCA	TTTATTCACT	AATACATTTT	ATTTGTGTTC	2100
TCTAATTTAA	AATTACCTTT	TCATCTTGCT	TGATTTTCCT	TCAGCTAAAT	TAGAAATTTG	2160
TAGTTTTTCC	CCTAAAAAAT	TCAATGGCAT	TCTTTCTTAT	AAATTACATT	CTCTGATTTT	2220
CTTGTCAGCC	TGCTTCAAAG	AAATCCATGT	GTTCAAAATG	CTTGCTCGCA	GTTTGCTCCA	2280
TACCAAATGG	TTGCTTAACC	CAAATATCTG	AGCAGCAAAT	TGAGCTGATC	CTTCTGGAGA	2340
AAGTACGGTT	GAACAGCCAA	GACCACTGGG	TAGTCGAAGA	GAAGACCACA	CATCCTGAAC	2400

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TCCCCAGTCT	GGTGTGAGGG	GAGGACAGCT	GATAACTGGA	TATGCAGTGT	TCCCAGACAT	2460
CACTGGTCCC	AAACCATTAC	TTCTGCCTGC	CACTGCCACA	AATACAGTAG	GAATGCCATC	2520
CCCTTCATAC	TCAGCTTTAA	TCCTCAGAGT	TTCATCTGGT	CCTTTATGCG	CAGATGTTAC	2580
TCGAAGTTCA	CATGGAATGC	CAAAATTTCC	ACAGGCCTTC	TTGATTTTTT	CACAGTGACC	2640
AAGATCAGAA	GTAGAGCCCA	TCAACACTAC	AACCCTGCAC	TGACTTTCTG	ATTTCAAAG	2700
CAACTCTACT	CTCTCTGCAA	CCCACTCAAA	GTTTTTCTTT	ACCATTGGA	GCCCTTCAGG	2760
AGTTACTTCT	TTGAGGTCCC	GATAAGACTG	TTTGTCTTTC	TGTTGGCTTC	GATCTCCTGA	2820
TGGCCAGAGT	CTCCAGGAAT	CATTGTCAAT	AACATCAGCA	AGAACAATTT	CTTTGGTGGT	2880
TACATCAACA	CCAAATTCAA	TCTTCATATC	AACCAGTGTA	CAATTCTGGG	GCAACCAGGA	2940
TTTCTCCAGT	ATTTCAAATA	TAGCCTGTGT	AGCATCTCGT	GCCGAATTCA	AAAAGCTT	2998

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAGCTTTTTG	TGAAAACCCCT	AGGATATGTC	CCCTCCCTCA	CCACACCCAA	CCCCCGCCC	60
CTGCCCCAGG	ACATGACGAT	GCCTCACACA	CACACACACA	CACACATACA	CACAAGGCCG	120
TGAGCTGCAC	GCAGGAACAT	GGGCTGCACT	CACGACAACA	TTGAAAAAAT	ATACATTATA	180
TATGTACACC	CGGGGCCCCC	ACGTCCCCTC	CCGTCCCCGC	AGCCTGGCCA	CACCAGGTCA	240
CGGAGGAGGG	GCCGGGGCTG	CAGGACCTCA	GGACTGCAAG	GGCAGGAAGG	GAAACAGGAC	300
AAGAAAGGAA	GGAAGTTGGA	AAGGAGGGAG	AAATGGGGTC	CCCAGACTGA	AATGGAAATG	360
AGGTGGGGCG	ATCATAAGAG	AAGCAGGGAC	GATGGTCCAG	CTGAGGGAGC	CCTGCAGAGG	420
GGGAAAAGCT	TCCCATGGAC	AGGAGAGAGA	AGGGAAGGGG	AGAGGAGAGG	GTTTCCTTCA	480
ATCCCACCCC	CAGCCCCAGC	CCCAGCCCCA	GCCATTGCAA	TCGTCACCCCT	CTCCCCAACA	540
CAGTGAGTGC	TAAGGGGGCA	GCTGCCATTG	GGGGTAGAAA	GGCAGCTGAA	GTCCAGCCCCA	600
CTTTCCAACC	CAGCCAGCCC	CAGTGCAAGG	GGCACACCAG	GAGCATGACA	GCCCAGAAGT	660
GAGGGATGGG	GGGCCGGGGG	AGGGGCAGGG	CGGACTCCAG	AGGGCCCCGT	GGGGTTTTGA	720
AATGAAAGGA	GGACTGGTTC	TGAAGCCTCT	CTCCCTCTTG	GTCTCTGTGT	TCCCAGAAAG	780
TCCTTCTCCC	ATGTCTGGAG	TGTCTGTTTC	ACCAGGGCAG	AATTCCCCCT	CTGCGTGGGG	840
AGAGGTGTAG	GCCTTAGTAG	CGGTGTGGGG	GGGTCTCGAT	GATGCGTCTC	TCGTGCTGCTC	900
TGGGGGAATC	GGCCACCTCC	GAGTCACTGC	TGTCCTCATC	CTCCTGCTGG	CCCCAACAG	960
CCCCCGTCAC	ACAGGACTGC	CGATTCTGGT	AGGACTCCAT	GGGGTTCACA	ATGATGGTGA	1020
GAGCTGAGTC	ATCCCAGAAG	AGGTCTGGGT	CCTTGGGGTC	ACTGGAGGCC	CCTGGAGGCC	1080
CGCCGGCCCC	TGAGACGCGG	CGGTGAAGGG	AATGGATGCG	CACCAGGCC	AGGACGACCA	1140
TGAGCACCAG	GAAGCCCACG	CACACCACAA	TGATGAGGGT	TGCGGCGCTG	GGTATCATGG	1200
AGTTTCTGTG	GGAGCTGGCT	AGGCTGTGTC	CAGCCATCTC	AGGCGGGGGC	TGGTGACCAC	1260
GGTGCAAGAA	CTGCTGGGAG	CTGAGCACGT	GGCTGGGGTG	GGCAACCCGG	TTCATGCTGT	1320
GCAGGACATT	GACCTCCACG	ATGAATTTCAT	TGCTGGAGTA	ACGGCCATTC	ATTTCCGAGC	1380
AGGAAAGCCG	GAACTTCCTG	GTGTAGAGGG	CAGCTCCGTG	TCGCAGCCGA	TAACGAGCCT	1440
GCCTCAGGAT	CTCTTCATAC	ACAGTGATGC	TCTCCACCCC	AGCAATAGTG	AGGTAGGCAG	1500
ATGTGTTGGT	GAGCTCCAGC	CCCCGCTGCT	GCAGAGAGGT	TGTGTCCAGG	AGCAGGCTTT	1560
CCCGCTCGGG	ATCCAGGTCA	TCCCCACCA	GAGAAATTTT	ACAGCCATCC	AGGTTGTGCA	1620
CAATCTCATC	CGACATGCGT	GTGTCTGTCA	CTGTGCCCTG	CCAATCTCA	TCCTTTTGG	1680
CCTCCACCTG	GTGAGAAATG	GAGCAGGTGA	TTTGAAGATC	AGGGAACAAA	GGGACGCCGT	1740
TGGTTCCCTC	AAAGTCCACA	GCTGGGCGGG	CAAAATGAGC	AGTGCCACTC	AGCAGGATCT	1800
GGGGGGCGTC	AGGCTGAAGG	ACGACCACGT	AGCCCTCCAC	TTCAGGGATG	GAGACGCAGG	1860
ACTCTTCGCT	GAAGCACTTG	ACAGCAGTGG	TGAGGCGCAG	GGGCCTGACG	CCGGGCGTGG	1920
CAAAGCGCAG	AGTGTTCATG	TAAGCCACAT	GCTGCAGGGC	ATGGTTGAAG	GTCTCCACAT	1980
CATCCCCCTC	CAGGGTGAGC	AGGGACTGTG	AGGGGTTTAC	GTGGACCTTC	ATGCCTTTGC	2040

CCAGGCTCTC	GAAATCCCTA	TAGTCCAGCC	CCTCCCAGCA	TGCATAGAGG	CACCTCGATGA	2100
CCTCGCGGCT	CTCCAGGCGA	CCTGAGCGCA	CGCTGAAAACC	AGCCAGGTAG	CCATGGAAGT	2160
AGTGGTGGAT	CGACAAAGGG	TCTCCTTGGG	TGGTGTCTGT	ACTGTTGTCT	CCCTTTTCCT	2220
TCTCTTTGTT	CTTCTCCTCA	GTCCAGCAGG	CCCCAATCAT	GAGAGCAGGC	TCCCTTCGGG	2280
GTGGGTGGAT	GAGGCCATTG	TCATGGATGA	GGGCAGGGTC	GAAGGAGATG	CCGTCGGTAT	2340
AGAGTGTGAC	TGTGGGGAAC	TCGAGGTTCA	GAGCGTAGTG	GTGCCACTCA	TCATCACAGA	2400
CCTGCTCCAG	CTTCCAGAGG	AACTTGACTG	GGCGGGCACT	CTCAAGCAGG	GGCCAGTAGA	2460
GGAAGGCAAT	CCTACAGCCG	TGGACAGTCA	GCGAGTAGTG	AGAGAAGCCG	TCCTCATTCT	2520
GGACAGTGTT	ACATACGATG	GTTTCCTCTT	CCTTCTTGCC	CTTGTTGGGA	GTTACGCCAT	2580
GCTTCATCCA	GAAGGACAGG	GTGAAGTGGT	CAGTGAAGGCT	GTCTTGGGGC	CCAGAGCCCA	2640
GCCCCTGGG	GCCACCCAGG	GGCACCTGCA	CAGCCTGGGT	GCCATTGAAC	CAGTAGATCA	2700
GGCTGCTGTC	CTGGCTGTAG	TGCACCGAGA	GTCTGCTGT	CCAGTTGGCA	TTGGGGCCAG	2760
GCATGGGCAA	CAGATCCACT	TCCCCAGTGG	CAGCACCACA	GAGTTTCCGC	AGCGCCCGCT	2820
CTGAGTAGTT	GTCACGGTCA	CAGCCCTTGG	CCACATGGCT	GGTCTGCAGC	TCTATGGTGG	2880
CCTGAATGTT	CCAGAGTGGT	TCATCACAGG	TCTCCAGGCG	GATACCAGGG	AACAAAGCCA	2940
AGCTCCCAGC	ACCTGGTGCA	TATTTCGATCC	TTTTGTTCCT	GCCTTGCCAG	CTGGGTTTAC	3000
AGGTGGGCTT	CACCTGAATC	TCCACCTCAG	CATCATCTGC	TGCCCCTGTC	TTCCCACAGT	3060
CATAAGCTGT	CACCTGTAAC	TTATAGAGCC	TCTACCACT	GTACTGCAGC	TTCTCTGTGT	3120
TCTCAATGTT	CCCGTCAATT	TCAATGAGGA	AAGGGGTGTT	GAGTGTGAGA	ATCTCATAGT	3180
AGCAGATCTG	GCTGTACTGG	GGGGAGCAGT	CACCGTCAAT	GGCTTCCACC	CGCAGGATGC	3240
GATCGTACAG	CTTCCCCTCT	GTCACAGCCG	CACGATACAG	CCGTTCCACA	AACACTGGGG	3300
CAAACCTCGT	CACATCGTTG	ACCCGCACAT	GCACAGTGGC	CTTGTGGGAC	TTCTTGGTGT	3360
TGGCCCCGTC	GGGGCCCTCG	CCACAGTCAT	AGGCCTGGAT	GGTGAAGGTG	TGTTCCCTCT	3420
GGGCCTCGCA	GTCCACAGGC	TCCTTGGCC	GGATCAGCCC	CTCTCCTGTC	GCCTTGTCAG	3480
GGATCACAGC	CTCAAAGGGC	ACCCAGAGCC	CATGGAGCCG	GAAGCCGCAG	ATCTCACCTG	3540
CATAGCGCAG	CGGGGCATCC	TTGTCCAAGG	CAAAGAGTGG	TGGATTCACT	AGGACCGTGT	3600
TGTCATTCTC	CATGACGATG	CCCTGGTACT	CTGCCTCAAT	CCATGGCTTG	TGCTTGTGGG	3660
CTTTGTTACA	GGAGCAGGAC	GCGAGCAGAG	AGGCCAGCAG	AAGGGGCAGC	AGCAGGAGGG	3720
TCATGGTGC	GCGTGGGGCA	GGGCAGGGCC	AGGCGTTTGC	CTCCCCTGGG	AGCCTCCAGC	3780
CTGCGGATTC	CACCTTGCGG	GAGGGATACA	GGGGGGGAAA	ACCAAAATAA	AACGTCAAAT	3840
AAATTGTGTA	GGAGGAGTCC	AGCTTAGGAC	CGGGCCAGAG	CCAGGCCAGG	CTCGGGGAGG	3900
GGGCCTCTGC	AGGTTACAGG	GATCACTGCT	GCCACCACCG	CCACCCTGGG	AGCCAGTTAT	3960
TTTGCCATGG	CCTTGATTGC	AACAGCTGCC	TCCTCTGTCA	TGGCAGACAG	CACCCGTGATC	4020
AGGATCTCTT	CTCCACAGTC	GTACTTCTGC	TCAATCTCCT	TGCCAAGGTC	TCCCTCAGGG	4080
ATACGAAGGT	CCTCTCGTAC	CTCCCCGCTG	TCCTGGAGCA	GTGATAGGTA	CCCATCCTGG	4140
ATCTTTGGAT	CC					4152

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGATCCAAAG	ATTCGGCACG	AGTGGCCACA	TCATGAACCT	CCAGGCCAG	CCCAAGGCTC	60
AGAACAAGCG	GAAAGCTTGC	CTCTTTGGGG	GCCAGGAACC	AGCTCCCAAG	GAGCAGCCCC	120
CTCCCCTGCA	GCCCCCCCAG	CAGTCCATCA	GAGTGAAGGA	GGAGCAGTAC	CTCGGGCACG	180
AGGGTCCAGG	AGGGGCAGTC	TCCACCTCTC	AGCCTGTGGA	ACTGCCCCCT	CCTAGCAGCC	240
TGGCCCTGCT	GAACTCTGTG	GTGTATGGGC	CTGAGCGGAC	CTCAGCAGCC	ATGCTGTCCC	300
AGCAGGTGGC	CTCAGTAAAG	TGGCCCAACT	CTGTGATGGC	TCCAGGGCGG	GGCCCGGAGC	360
GTGGAGGAGG	TGGGGGTGTC	AGTGACAGCA	GCTGGCAGCA	GCAGCCAGGC	CAGCCTCCAC	420
CCCATTC AAC	ATGGA ACTGC	CACAGTCTGT	CCCTCTACAG	TGCAACCAAG	GGGAGCCCGC	480

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ATCCTGGAGT	GGGAGTCCCG	ACTTACTATA	ACCACCCTGA	GGCACTGAAG	CGGGAGAAAG	540
CGGGGGGCCC	ACAGCTGGAC	CGCTATGTGC	GACCAATGAT	GCCACAGAAG	GTGCAGCTGG	600
AGGTAGGGCG	GCCCCAGGCA	CCCCTGAATT	CTTTCCACGC	AGCCAAGAAA	CCCCCAAACC	660
AGTCACTGCC	CCTGCAACCC	TTCCAGCTGG	CATTTCGGCCA	CCAGGTGAAC	CGGCAGGTCT	720
TCCGGCAGGG	CCCACCGCCC	CCAAACCCGG	TGGCTGCCTT	CCCTCCACAG	AAGCAGCAGC	780
AGCAGCAGCA	ACCACAGCAG	CAGCAGCAGC	AGCAGCAGGC	AGCCCTACCC	CAGATGCCGC	840
TCTTTGAGAA	CTTCTATTCC	ATGCCACAGC	AACCCTCGCA	GCAACCCAG	GACTTTGGCC	900
TGCAGCCAGC	TGGGCCACTG	GGACAGTCCC	ACCTGGCTCA	CCACAGCATG	GCACCCTACC	960
CCTTCCCCCC	CAACCCAGAT	ATGAACCCAG	AACTGCGCAA	GGCCCTTCTG	CAGGACTCAG	1020
CCCCGCAGCC	AGCGCTACCT	CAGGTCCAGA	TCCCCTTCCC	CCGCCGCTCC	CGCCGCCTCT	1080
CTAAGGAGGG	TATCCTGCCCT	CCCAGCGCCC	TGGATGGGGC	TGGCACCCAG	CCTGGGCAGG	1140
AGGCCACTGG	CAACCTGTTT	CTACATCACT	GGCCCTTGCA	GCAGCCGCCA	CCTGGCTCCC	1200
TGGGGCAGCC	CCATCCTGAA	GCTCTGGGAT	TCCCGCTGGA	GCTGAGGGAG	TCGCAGCTAC	1260
TGCCTGATGG	GGAGAGACTA	GCACCCAATG	GCCGGGAGCG	AGAGGCTCCT	GCCATGGGCA	1320
GCGAGGAGGG	CATGAGGGCA	GTGAGCACAG	GGGACTGTGG	GCAGGTGCTA	CGGGGCGGAG	1380
TGATCCAGAG	CACGCGACGG	AGGCGCCGGG	CATCCCAGGA	GGCCAATTTG	CTGACCCTGG	1440
CCCAGAAGGC	TGTGGAGCTG	GCCTCACTGC	AGAATGCAAA	GGATGGCAGT	GGTTCTGAAG	1500
AGAAGCGGAA	AAGTGTATTG	GCCTCAACTA	CCAAGTGTGG	GGTGGAGTTT	TCTGAGCCTT	1560
CCTTAGCCAC	CAAGCGAGCA	CGAGAAGACA	GTGGGATGGT	ACCCCTCATC	ATCCCAGTGT	1620
CTGTGCCTGT	GCGAACTGTG	GACCCAACCTG	AGGCAGCCCA	GGCTGGAGGT	CTTGATGAGG	1680
ACGGGAAGGG	TCTTGAACAG	AACCCTGCTG	AGCACAAAGCC	ATCAGTCATC	GTCACCCGCA	1740
GGCGGTCCAC	CCGAATCCCC	GGGACAGATG	CTCAAGCTCA	GGCGGAGGAC	ATGAATGTCA	1800
AGTTGGAGGG	GGAGCCTTCC	GTGCGGAAAC	CAAAGCAGCG	GCCCAGGCC	GAGCCCCTCA	1860
TCATCCCCAC	CAAGGCGGGC	ACTTTCATCG	CCCCTCCCCT	CTACTCCAAC	ATCACCCCAT	1920
ACCAGAGCCA	CCTGCGCTCT	CCCGTGCGCC	TAGCTGACCA	CCCCTCTGAG	CGGAGCTTTG	1980
AGCTACCTCC	CTACACGCCG	CCCCCATCC	TCAGCCCTGT	GCGGGAAGGC	TCTGGCCTCT	2040
ACTTCAATGC	CATCATATCA	ACCAGCACCA	TCCCTGCCCC	TCCTCCCATC	ACGCCTAAGA	2100
GTGCCCATCG	CACGCTGCTC	CGGACTAACA	GTGCTGAAGT	AACCCCGCCT	GTCTCTCTG	2160
TGATGGGGGA	GGCCACCCCA	GTGAGCATCG	AGCCACGGAT	CAACGTGGGC	TCCCGGTTCC	2220
AGGCAGAAAT	CCCCTTGATG	AGGGACCGTG	CCCTGGCAGC	TGCAGATCCC	CACAAGGCTG	2280
ACTTGGTGTG	GCAGCCATGG	GAGGACCTAG	AGAGCAGCCG	GGAGAAGCAG	AGGCAAGTGG	2340
AAGACCTGCT	GACAGCCGCC	TGCTCCAGCA	TTTTCCCTGG	TGCTGGCACC	AACCAGGAGC	2400
TGGCCCTGAC	CTGTCTGCAC	GAATCCAGAG	GAGACATCCT	GGAAACGCTG	AATAAGCTGC	2460
TGCTGAAGAA	GCCCCTGCGG	CCCCACAACC	ATCCGCTGGC	AACTTATCAC	TACACAGGCT	2520
CTGACCAGTG	GAAGATGGCC	GAGAGGAAGC	TGTTCAACAA	AGGCATTGCC	ATCTACAAGA	2580
AGGATTTCTT	CCTGGTGCAG	AAGCTGATCC	AGACCAAGAC	CGTGGCCCAG	TGCGTGGAGT	2640
TCTACTACAC	CTACAAGAAG	CAGGTGAAAA	TCGGCCGCAA	TGGGACTCTA	ACCTTTGGGG	2700
ATGTGGATAC	GAGCGATGAG	AAGTCGGCCC	AGGAAGAGGT	TGAAGTGGAT	ATTAAGACTT	2760
CCCAAAGTT	CCCAAGGGTG	CCTCTTCCCA	GAAGAGAGTC	CCCAAGTGAA	GAGAGGCTGG	2820
AGCCCAAGAG	GGAGGTGAAG	GAGCCCAGGA	AGGAGGGGGA	GGAGGAGGTG	CCAGAGATCC	2880
AAGAGAAGGA	GGAGCAGGAA	GAGGGGCGAG	AGCGCAGCAG	GCGGGCAGCG	GCAGTCAAAG	2940
CCACGCAGAC	ACTACAGGCC	AATGAGTCGG	CCAGTGACAT	CCTCATCCTC	CGGAGCCACG	3000
AGTCCAACGC	CCCTGGGTCT	GCCGGTGGCC	AGGCCTCGGA	GAAGCCAAGG	GAAGGGACAG	3060
GGAAGTCACG	AAGGGCACTA	CCTTTTTTCAG	AAAAAAAAAA	AAAAAACAA	AAAGCTT	3117

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

09700354.1.1.300

GAATTCGGCA	CGAGGTCAGT	TTCCTGTGGA	ACACAGAGGC	TGCCTGTCCC	ATTCAGACAA	60
CGACGGATAC	AGACCAGGCT	TGCTCTATAA	GGGATCCCCA	CAGTGGATTT	GTGTTTAATC	120
TTAATCCGCT	AAACAGTTCG	CAAGGATATA	ACGTCTCTGG	CATTGGGAAG	ATTTTTATGT	180
TTAATGTCTG	CGGCACAATG	CCTGTCTGTG	GGACCATCCT	GGGAAAACCT	GCTTCTGGCT	240
GTGAGGCAGA	AACCCAAACT	GAAGAGCTCA	AGAATTGGAA	GCCAGCAAGG	CCAGTCGGAA	300
TTGAGAAAAG	CCTCCAGCTG	TCCACAGAGG	GCTTCATCAC	TCTGACCTAC	AAAGGGCCTC	360
TCTCTGCCAA	AGGTACCGCT	GATGCTTTTA	TCGTCCGCTT	TGTTTGCAAT	GATGATGTTT	420
ACTCAGGGCC	CCTCAAATTC	CTGCATCAAG	ATATCGACTC	TGGGCAAGGG	ATCCGAAACA	480
CTTACTTTGA	GTTTGAAACC	GCGTTGGCCT	GTGTTCCCTC	TCCAGTGGAC	TGCCAAGTCA	540
CCGACCTGGC	TGGAAATGAG	TACGACCTGA	CTGGCCTAAG	CACAGTCAGG	AAACCTTGGA	600
CGGCTGTTGA	CACCTCTGTC	GATGGGAGAA	AGAGGACTTT	CTATTTGAGC	GTTTGCAATC	660
CTCTCCCTTA	CATTCTTGGA	TGCCAGGGCA	GCGCAGTGGG	GTCTTGCTTA	GTGTCAGAAG	720
GCAATAGCTG	GAATCTGGGT	GTGGTGCAGA	TGAGTCCCCA	AGCCGCGGCG	AATGGATCTT	780
TGAGCATCAT	GTATGTCAAC	GGTGACAAGT	GTGGGAACCA	GCGCTTCTCC	ACCAGGATCA	840
CGTTTGAGTG	TGCTCAGATA	TCGGGCTCAC	CAGCATTTCA	GCTTCAGGAT	GGTTGTGAGT	900
ACGTGTTTAT	CTGGAGAACT	GTGGAAGCCT	GTCCCGTTGT	CAGAGTGGAA	GGGGACAAC	960
GTGAGGTGAA	AGACCCAAGG	CATGGCAACT	TGTATGACCT	GAAGCCCCTG	GGCCTCAACG	1020
ACACCATCGT	GAGCGCTGGC	GAATACACTT	ATTACTTCCG	GGTCTGTGGG	AAGCTTTCCT	1080
CAGACGTCTG	CCCCACAAGT	GACAAGTCCA	AGGTGGTCTC	CTCATGTCTG	GAAAAGCGGG	1140
AACCGCAGGG	ATTTACAAAA	GTGGCAGGTC	TCCTGACTCA	GAAGCTAACT	TATGAAAATG	1200
GCTTGTTAAA	AATGAACTTC	ACGGGGGGGG	ACACTTGCCA	TAAGGTTTAT	CAGCGCTCCA	1260
CAGCCATCTT	CTTCTACTGT	GACCGCGGCA	CCCAGCGGCC	AGTATTTCTA	AAGGAGACTT	1320
CAGATTGTTC	CTACTTGTTC	GAGTGGCGAA	CGCAGTATGC	CTGCCCACCT	TTCGATCTGA	1380
CTGAATGTTC	ATTCAAAGAT	GGGGCTGGCA	ACTCCTTCGA	CCTCTCGTCC	CTGTCAAGGT	1440
ACAGTGACAA	CTGGGAAGCC	ATCACTGGGA	CGGGGGACCC	GGAGCACTAC	CTCATCAATG	1500
TCTGCAAGTC	TCTGGCCCCG	CAGGCTGGCA	CTGAGCCGTG	CCCTCCAGAA	GCAGCCGCGT	1560
GTCTGCTGGG	TGGCTCCAAG	CCCCTGAACC	TCGGCAGGGT	AAGGGACGGA	CCTCAGTGGA	1620
GAGATGGCAT	AATTGTCCCTG	AAATACGTTG	ATGGCGACTT	ATGTCCAGAT	GGGATTCGGA	1680
AAAAGTCAAC	CACCATCCGA	TTCACCTGCA	GCGAGAGCCA	AGTGAAGTCC	AGGCCCATGT	1740
TCATCAGCGC	CGTGGAGGAC	TGTGAGTACA	CCTTTGCCCTG	GCCCACAGCC	ACAGCCTGTC	1800
CCATGAAGAG	CAACGAGCAT	GATGACTGCC	AGGTCACCAA	CCCAAGCACA	GGACACCTGT	1860
TTGATCTGAG	CTCCTTAAGT	GGCAGGGCGG	GATTACACAGC	TGCTTACAGC	GAGAAGGGGT	1920
TGGTTTACAT	GAGCATCTGT	GGGGAGAATG	AAAAGTCCCC	TCCTGGCGTG	GGGGCCTGCT	1980
TTGGACAGAC	CAGGATTAGC	GTGGGCAAGG	CCAACAAGAG	GCTGAGATAC	GTGGACAGG	2040
TCCTGCAGCT	GGTGTACAAG	GATGGGTCCC	CTTGTCCCTC	CAAATCCGGC	CTGAGCTATA	2100
AGAGTGTGAT	CAGTTTCGTG	TGCAGGCCTG	AGGCCGGGCC	AACCAATAGG	CCCATGCTCA	2160
TCTCCCTGGA	CAAGCAGACA	TGCACTCTCT	TCTTCTCCTG	GCACACGCCG	CTGGCCTGCG	2220
AGCAAGCGAC	CGAATGTTCC	GTGAGGAATG	GAAGCTCTAT	TGTTGACTTG	TCTCCCCTTA	2280
TTCATCGCAC	TGGTGGTTAT	GAGGCTTATG	ATGAGAGTGA	GGATGATGCC	TCCGATACCA	2340
ACCCTGATTT	CTACATCAAT	ATTTGTCAGC	CACTAAATCC	CATGCACGGA	GTGCCCTGTC	2400
CTGCCGGAGC	CGCTGTGTGC	AAAGTTCCTA	TTGATGGTCC	CCCCATAGAT	ATCGGCCGGG	2460
TAGCAGGACC	ACCAATACTC	AATCCAATAG	CAAATGAGAT	TTACTTGAAT	TTTGAAAGCA	2520
GTACTCCTTG	CCAGGAATTC	AGTTGTAAAT	AAAATTGAAC	CTGCTCAACA	GCTGAGGGAG	2580
ACTAGAAATG	ATGGGTCCAT	ATCCTGGTGC	ATTGTCATAC	AATTCAAACA	ATGGTGCAGC	2640
TACCAGCTTG	TAATTTTTAG	GGACTGCAAA	CAAGGCTTTT	TCTTGAAGCT	GAACCAGAAA	2700
CAACTTCTTA	TGTTCCCTAG	GCTTTGTAAT	ATGTGCAGGA	ATATATGGAT	ACTGAGGAGG	2760
TTCAAAATTT	GGTCTCCACC	AGTTACCAAT	GCAATCGTCA	ATGACCCAGT	CTTGCAAAAC	2820
TCCATCCTGA	CGACCCAGTA	TCTCTGTCAT	TAAGCGTTTT	AGTCCTTCAA	CTTCATCTTC	2880
TCCTGGGTTA	AGTTCACCAC	CAGGTAGTTT	GAAGAAAGTT	GTTCCCAGCT	GCAGCAGTAA	2940
CACATGGGGT	AGCCGGTGCT	CATGTACAAT	CAGAACCCCT	TCTACAGTCC	TCCTCATTCC	3000
AATTTTATCA	AATTCCTCCC	TCATGCGCTG	AAATCTGGCT	GCAACAGAGC	TGTCCTTCTC	3060
GTAGAGGGGC	TCTTTTGTAC	CAAAAGTATA	ATTGGTAAGA	GGGTACAGGT	TGATGGTGCG	3120
CTCCAGGGTG	AGGGGCTTCG	TCTGCTGGAT	GTACTTGTGT	CCGAACTGAG	TGACCCCGCG	3180
GGGCCAGCCG	GTCTGCGAGC	GATTGGGCGG	TACCACAGAC	ATGCTGGCGA	GCTCCGGCGC	3240
TGACGGCGAG	CAGAAAGTGG	CAGGCAGGGT	AGACTTTCCC	CGTGCGGGAA	GCCTCGTGCC	3300
GAATTC						3306

(2) INFORMATION FOR SEQ ID NO:8:



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4218 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTCGGCA CGAGAATGGA TCAACCTCAA CAACACGTTA AAGCTAGACG AAAGAAGTAA 60  
TACACAGTGT ATGAGTCTCA CATGAAATAC CCGGATGTAA ATCCAAAGAA ACAGGAAGCA 120  
GATTGGTGGT TGCCAGGGAC AAGGGCGGTG GGAGGAGAAA ATGGAGAGTA ACGGGACTTT 180  
ACTTTTGGAG TGATGAGAAT GTTTTGGAGC TAGATAGAAG TGGTGGTTGT ACACCATTGT 240  
GGATGTACTA CCACTTAATT GTTCACTTAA AAAGTTAATT TATGTGAATT GCATCTTAAT 300  
TAAAAACAAG GATAACATTC CAACTCCTGG ACATTATCCT TCCTTTCCAT TTGATGTCAG 360  
GCCCCTGTGA GAATTCTCAT CCGGTTTGGT CACTGCACCT AAGATGTGGA GAAATTAGGA 420  
CGCACAGTTA AGAGGAAGGA TAACACTGAT TAAGGTAGTG CTTTTCTAGG TTCCCTTAA 480  
ACAATTTAAC AGATGGATAG TGGCACCCTT TACGAGATGG AAAAACCAGC GGAAGGAAGA 540  
TTTGGGGGAG AAGTTAAGTT TGTCTTGGGC CTGTGTTTTG CAACCTGAGT GTAAAAGACA 600  
TATGTTAAGT CTTCACTGGC GAAACACTAA AACTAGAAAT GGATCAGAAT TTTATCTTTG 660  
GATGTGACTT CTCAAGGATG GTCTTGTGAC TTCAGTGCCT GGTCAAATGA CAAGATGGGC 720  
AATCTTTTCC TGAAGGTCCA AGCACCTGAA CGTGGCAGGG TGACCCGATT CCGATTTGCT 780  
TAGAACAATC CTAGTTCATG CCTATTGTCC CTCATGTAAT TAATATCACT CTCAAAATGT 840  
CTCATTTTGT GCAATAAATT CTGCAACGTG ATGGCGCGAC TCTCGCGGCC CGAGCGGCCG 900  
GACCTTGTCT TCGAGGAAGA GGACCTCCCC TATGAGGAGG AAATCATGCG GAACCAATTC 960  
TCTGTCAAAT GCTGGCTTCA CTACATCGAG TTCAAACAGG GCGCCCCGAA GCCCAGGCTC 1020  
AATCAGCTAT ACGAGCGGGC ACTCAAGCTG CTGCCCTGCA GCTACAAACT CTGGTACCGA 1080  
TACCTGAAGG CGCGTCGGGC ACAGGTGAAG CATCGCTGTG TGACCGACCC TGCTATGAA 1140  
GATGTCAACA ACTGTGATGA GAGGGCCTTT GTGTTTATGC ACAAGATGCC TCGTCTGTGG 1200  
CTAGATTACT GCCAGTTCCT CATGGACCAG GGGCGCGTCA CACACACCCG CCGCACCTTC 1260  
GACCGTGCCC TCCGGGCACT GCCCATCACG CAGCACTCTC GAATTTGGCC CCTGTATCTG 1320  
CGCTTCCTGC GTCACACCC ACTGCCTGAG ACAGCTGTGC GAGGCTATCG GCGCTTCCTC 1380  
AAGCTGAGTC CTGAGAGTGC AGAGGAGTAC ATTGAGTACC TCAAGTCAAG TGACCGGCTG 1440  
GATGAGGCCG CCCAGCGCCT GGCCACCGTG GTGAACGACG AGCGTTTCGT GTCTAAGGCC 1500  
GGCAAGTCCA ACTACCAGCT GTGGCACGAG CTGTGCGACC TCATCTCCCA GAATCCGGAC 1560  
AAGGTACAGT CCCTCAATGT GGACGCCATC ATCCGCGGGG GCCTCACCCG CTTACCCGAC 1620  
CAGCTGGGCA AGCTCTGGTG TTCTCTCGCC GACTACTACA TCCGACGCGG CCATTTTCGAG 1680  
AAGGCTCGGG ACGTGTACGA GGAGGCCATC CGGACAGTGA TGACCGTGCG GGACTTCACA 1740  
CAGGTGTTTG ACAGCTACGC CCAGTTCGAG GAGAGCATGA TCGCTGCAAA GATGGAGACC 1800  
GCCTCGGAGC TGGGGCGCGA GGAGGAGGAT GATGTGGACC TGGAGCTGCG CCTGGCCCGC 1860  
TTGAGCAGC TCATCAGCCG GCGGCCCTG CTCCTCAACA GCGTCTTGCT GCGCCAAAAC 1920  
CCACACCACG TGCACGAGTG GCACAAGCGT GTCGCCCTGC ACCAGGGCCG CCCCCGGGAG 1980  
ATCATCAACA CCTACACAGA GGCTGTGCAG ACGGTGGACC CCTTCAAGGC CACAGGCAAG 2040  
CCCCACACTC TGTGGGTGGC GTTTGCCAAG TTTTATGAGG ACAACGGACA GCTGGACGAT 2100  
GCCCCTGTCA TCCTGGAGAA GGCCACCAAG GTGAACTTCA AGCAGGTGGA TGACCTGGCA 2160  
AGCGTGTGGT GTCAGTGCAG AGAGCTGGAG CTCCGACACG AGAACTACGA TGAGGCCCTT 2220  
CGGCTGCTGC GAAAGGCCAC GCGCTGCCT GCCCGCCGGG CCGAGTACTT TGATGGTTCA 2280  
GAGCCCGTGC AGAACCGCGT GTACAAGTCA CTGAAGGTCT GGTCCATGCT CGCCGACCTG 2340  
GAGGAGAGCC TCGGCACCTT CCAGTCCACC AAGGCCGTGT ACGACCGCAT CCTGGACCTG 2400  
CGTATCGCAA CACCCAGAT CGTCATCAAC TATGCCATGT TCCTGGAGGA GCACAAGTAC 2460  
TTGAGGAGA GCTTCAAGGC GTACGAGCGC GGCATCTCGC TGTTCAAGTG GCCCAACGTG 2520  
TCCGACATCT GGAGCACCTA CCTGACCAA TTCAATGCCC GCTATGGGGG CCGCAAGCTG 2580  
GAGCGGGCAC GGGACCTGTT TGAACAGGCT CTGACCGGCT GCGCCCAAA ATATGCAAG 2640  
ACCTTGTACC TGCTGTACGC ACAGCTGGAG GAGGAGTGGG GCCTGGCCCG GCATGCCATG 2700  
GCCGTGTACG AGCGTGCCAC CAGGGCCGTG GAGCCCGCCC AGCAGTATGA CATGTTCAAC 2760

ATCTACATCA	AGCGGGCGGC	CGAGATCTAT	GGGGTCACCC	ACACCCGCGG	CATCTACCAG	2820
AAGGCCATTG	AGGTGCTGTC	GGACGAGCAC	GCGCGTGAGA	TGTGCCTGCG	GTTTGCAGAC	2880
ATGGAGTGCA	AGCTCGGGGA	GATTGACCGC	GCCCCGGCCA	TCTACAGCTT	CTGCTCCCAG	2940
ATCTGTGACC	CCCGGACGAC	CGGCGCGTTC	TGGCAGACGT	GGAAGGACTT	TGAGGTCCGG	3000
CATGGCAATG	AGGACACCAT	CAAGGAAATG	CTGCGTATCC	GGCGCAGCGT	GCAGGCCACG	3060
TACAACACGC	AGGTCAACTT	CATGGCCTCG	CAGATGCTCA	AGGTCTCGGG	CAGTGCCACG	3120
GGCACCCTGT	CTGACCTGGC	CCCTGGGCAG	AGTGGCATGG	ACGACATGAA	GCTGCTGGAA	3180
CAGCGGGCAG	AGCAGCTGGC	GGCTGAGGCG	GAGCGTGACC	AGCCCTTGCG	CGCCCAGAGC	3240
AAGATCCTGT	TCGTGAGGAG	TGACGCCTCC	CGGGAGGAGC	TGGCAGAGCT	GGCACAGCAG	3300
GTCAACCCCG	AGGAGATCCA	GCTGGGCGAG	GACGAGGACG	AGGACGAGAT	GGACCTGGAG	3360
CCCAACGAGG	TTCGGCTGGA	GCAGCAGAGC	GTGCCAGCCG	CAGTGTTTGG	GAGCCTGAAG	3420
GAAGACTGAC	CCGTCCCCTC	GTGCCGAATT	CGGCACGAGC	AAGACCAGCC	CCCAGATCAT	3480
TTGCCTCAAA	GGTTTTCCCT	CGAAGTCACA	AATGTTTCAA	GGAATCTCAA	ATTTTACAAA	3540
GTTTGAAGTG	TGGGCATTGG	TGGCCTGTGG	CTGTGTCCTC	TCTCTGTAGC	TGTTTTCTCC	3600
CTACATCCCT	GAAAGGAAGT	TGAGCCTGCT	CCTCCATCCG	CAGACCTCCC	TTTCCAGCGC	3660
CCAGGGCATG	GGGTGCTGTG	AGGGCAGCAT	GCTAGGTGTG	ACCGTGCTCC	TGGCCTCCAG	3720
GCCCGTGTCC	CTCTGTCTC	TAGCCCACTA	AGGCCCTGGC	CCATTTGTGC	TAAACAGGCA	3780
GTCGGACCTA	GAAAGAGCAG	ACAATCTCTC	TGGGTCACCA	GTCTGGCTAG	GAGCTGGTCT	3840
CCTGACTGGG	ATCCAGGCCT	TCTCCCCTGC	CCATGTGAAT	TCCCAGGGGC	AGAGCCTGAA	3900
ATGTTGAACA	CAGCACTGGC	CAAAGAGATG	TCACCGTGGG	AACCGAGGCT	CTCTTCTCCT	3960
CCTGCCTGCT	TTCGTGGGTT	CAGAGTAGCT	GAGGCTTGTC	TGAGAGGAGT	TGGAGTGCTG	4020
GTTTTACCCC	TGGTTGGTGT	GCTTTGCTTT	GAGGGCACTT	AGAAAGCCCA	GCCCAGCCCT	4080
TGCTCCTGCC	CTGCACACAG	CGGAGCGACT	TTTCTAGGTA	TGCTCTTGAT	TTCTGCAGAA	4140
GCAGCAGGTG	GCATGGAGCC	AAGAGGAAGT	GTGACTGAAA	CTGTCCACTC	ATAGCCCGGC	4200
TGCCGTATTG	AGAGGGCT					4218

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1187 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAGCTCGCGC	GCCTGCAGGT	CGACACTAGT	GGATCCAAAG	AATTCGGCAC	GAGGGAAACT	60
CAACGGTGTA	CGAGTGAGAG	ACAGGGACAG	AGCCCTCTGT	GGTGGAACGA	CCCCACCTCG	120
AGGAGCTTCC	TGAGCAGGTG	GCAGAAAGATG	CGATTGACTG	GGGCGACTTT	GGGGTAGAGG	180
CAGTGTCTGA	GGGGACTGAC	TCTGGCATCT	CTGCCGAGGC	TGCTGGAATC	GACTGGGGCA	240
TCTTCCCGBA	ATCAGATTCA	AAGGATCCTG	GAGGTGATGG	GATAGACTGG	GGAGACGATG	300
CTGTTGCTTT	GCAGATCACA	GTGCTGGAAG	CAGGAACCCA	GGCTCCAGAA	GGTGTGCCA	360
GGGGCCCAGA	TGCCCTGACA	CTGCTTGAAT	ACACTGAGAC	CCGGAATCAG	TTCCTTGATG	420
AGCTCATGGA	GCTTGAGATC	TTCTTAGCCC	AGAGAGCAGT	GGAGTTGAGT	GAGGAGGCAG	480
ATGTCCTGTC	TGTGAGCCAG	TTCCAGCTGG	CTCCAGCCAT	CCTGCAGGGC	CAGACCAAAG	540
AGAAGATGGT	TACCATGGTG	TCAGTGCTGG	AGGATCTGAT	TGGCAAGCTT	ACCAGTCTTC	600
AGCTGCAACA	CCTGTTTATG	ATCCTGGCCT	CACCAAGGTA	TGTGGACCGA	GTGACTGAAT	660
TCCTCCAGCA	AAAGCTGAAG	CAGTCCCAGC	TGCTGGCTTT	GAAGAAAGAG	CTGATGGTGC	720
AGAAGCAGCA	GGAGGCACTT	GAGGAGCAGG	CGGCTCTGGA	GCCTAAGCTG	GACCTGCTAC	780
TGGAGAAGAC	CAAGGAGCTG	CAGAAGCTGA	TTGAAGCTGA	CATCTCCAAG	AGGTACAGCG	840
GGCGCCCTGT	GAACCTGATG	GGAACCTCTC	TGTGACACCC	TCCGTGTTCT	TGCCGTGCCA	900
TCTTCTCCGC	TTTTGGGATG	AAGATGATAG	CCAGGGCTGT	TGTTTTGGGG	CCCTTCAAGG	960
CAAAAGACCA	GGCTGACTGG	AAGATGGAAA	GCCACAGGAA	GGAAGCGGCA	CCTGATGGTG	1020
ATCTTGGCAC	TCTCCATGTT	CTCTACAAGA	AGCTGTGGTG	ATTGGCCCTG	TGGTCTATCA	1080
GGCGAAAACC	ACAGATTCTC	CTTCTAGTTA	GTATAGCGCA	AAAAGCTTCT	CGAGAGTACT	1140

TCTAGAGCGG CCGCGGGCCC ATCGATTTTC CACCCGGGTG GGGTACC

1187

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCCTCACTAA	AGGGAACAAA	AGCTGGAGCT	CGCGCGCCTG	CAGGTCGACA	CTAGTGGATC	60
GAAAGTTCGT	TACGCCAAGC	TCGAAATTAA	CTCTGGGCTG	ACCCATAAAC	ATTTGTCTGA	120
TCTAGGATAT	AGTTGCGTTT	CTTGCGGGCA	GCAATCTGGA	TGAGGCGGTT	GAGGCACTGG	180
GTGGCCTGCT	GGATCAGGAC	ATCCCAGCGG	CCAGCATAGT	TCCGCTGCCG	GCGTAGGCCC	240
ATCACCCGCA	TCTTATCCAT	GATGGCATTG	GTACCCAGGA	TGTTGTACTT	CTTGGAAGGG	300
TTGGAGGCTG	CATGTTTGAT	GGCCCATGTG	GTCTTGCCAG	CAGCAGGCAG	GCCCACCATC	360
ATCAGAATCT	CACATTCTGC	CTTGCTCTTT	GGTCCAACGG	TGCCCCGGAT	ACGCTCACTA	420
AGGGGAAGGT	GCTGGATGAA	GGTAAACCCC	GGGAGGACAG	AACAGTAGGG	CTCTGCTCTC	480
TGTCCGAAGT	TGAACTCCAC	TGCGCAATTC	TTCACCAGGA	CATGAGGATA	GAGGGCCTGA	540
CCCCCAAGG	CTTCCTTCTG	GATTCGAAAA	GCAATGCCCA	TCCACTTTCC	ATTCTTG GTA	600
AAAGACAGTT	CCACGTCATT	TCCACATTCA	AAATCCGCAA	AGCAGCCAAT	CACCGGAGAG	660
CTCTGCGGTG	CTAGGAGAGC	GGCTGGGCCC	GCAGACTGGG	GGGAAAGCTC	CGCAGCCGCA	720
GTGGGCCCCA	GGATCAGGCC	CCGCGTGGCC	TGGAGAAGCC	CAGTCTGGGC	TGGAGCGGGA	780
GCTGGACAGT	GTGGCCTTGC	GTTCGCCCCC	GGGAGCGCTG	CGAGTGTGCG	GGCCTCGGGT	840
GGATTTGCTG	AGCACCAATA	CCTCACGGTT	GCCAACCTGG	GGTTTTAGCT	CCCTTG GTTT	900
TAATCCCCTA	GGGGCGGGTG	GGGGCACGGG	AGGAAGGATG	GGCCAGCTGG	GTGCAATCCT	960
GCTGTAAGCC	AGCCATTCTT	TGATTTCTTA	GAATTAACTA	AACGGTCGCG	CCGGAGGCCG	1020
CGGGGGCCGG	AGCGGAGCAG	CCGCGGCTGA	GGTTCCCAG	TCGGCCGCTC	GGGGCTGCGC	1080
TCCGCCGCCG	GGACCCCGGC	CTCTGGCCGC	GCCGGCTCCG	GCCTCCGGGG	GGGCCGGGGC	1140
CGCCGGGACA	TGGTGCCAGT	CGCACCCCTT	CCCCGCCGCC	GCTGAGCTCG	CCGGCCGCGC	1200
CCGGGCTGGG	ACGTCCGAGC	GGGAAGATGT	TTTCCGCCCT	GAAGAAGCTG	GTGGGGTCGG	1260
ACCAGGCCCC	GGGCCGGGAC	AAGAACATCC	CCGCCGGGCT	GCAGTCCATG	AACCAGGCGT	1320
TGCAGAGGCG	CTTCGCCAAG	GGGGTGCACT	ACAACATGAA	GATAGTGATC	CGGGGAGACA	1380
GGAACACGGG	CAAGACAGCG	CTGTGGCACC	GCCTGCAGGG	CCGGCCGTTC	GTGGAGGAGT	1440
ACATCCCCAC	ACAGGAGATC	CAGGTCACCA	GCATCCACTG	GAGCTACAAG	ACCACGGATG	1500
ACATCGTGAA	GGTTGAAGTC	TGGGATGTAG	TAGACAAAGG	AAAATGCAAA	AAGCGAGGCG	1560
ACGGCTTAAA	GATGGAGAAC	GACCCCCAGG	AGNCGGAGTC	TGAAATGGCC	CTGGATGCTG	1620
AGTTCCTGGA	CGTGTAACAAG	AACTGCAACG	GGGTGGTCAT	GATGTTGAC	ATTACCAAGC	1680
AGTGGACCTT	CAATTACATT	CTCCGGGAGC	TTCCAAAAGT	GCCCACCCAC	GTGCCAGTGT	1740
GCGTGCTGGG	GAATAACCGG	GACATGGGCG	AGCACCGAGT	CATCCTGCCG	GACGACGTGC	1800
GTGACTTCAT	CGACAACCTG	GACAGACCTC	CAGGTTCCCTC	CTACTTCCGC	TATGCTGAGT	1860
CTTCCATGAA	GAACAGCTTC	GGCCTAAAAGT	ACCTTCATAA	GTTCTTCAAT	ATCCCATTTT	1920
TGCAGCTTCA	GAGGGAGACG	CTGTTGCGGC	AGCTGGAGAC	GAACCAGCTG	GACATGGACG	1980
CCACGCTGGA	GGAGCTGTCTG	GTGCAGCAGG	AGACGGAGGA	CCAGAACTAC	GGCATCTTCC	2040
TGGAGATGAT	GGAGGCTCGC	AGCCGTGGCC	ATGCGTCCCC	ACTGGCGGCC	AACGGGCAGA	2100
GCCCATCCCC	GGGCTCCCAG	TCACCAGTCC	TGCCTGCACC	CGCTGTGTCC	ACGGGGAGCT	2160
CCAGCCCCGG	CACACCCAG	CCCGCCCCAC	AGCTGCCCCCT	CAATGCTGCC	CCACCATCCT	2220
CTGTGCCCCC	TGTACCACCC	TCAGAGGCCC	TGCCCCCACC	TGCGTGCCCC	TCAGCCCCCG	2280
CCCCACGGCG	CAGCATCATC	TCTAGGCTGT	TTGGGACGTC	ACCTGCCACC	GAGGACGCCC	2340
CTCCACCTCC	AGAGCCAGTC	CCGGCCGCAC	AGGGCCGAGC	AACGGTCCAG	AGTGTGGAGG	2400
ACTTTGTTCC	TGACGACCGC	CTGGACCGCA	GCTTCCTGGA	AGACACAACC	CCC GCCAGGG	2460
ACGAGAAGAA	GGTGGGGGCC	AAGGCTGCCC	AGCAGGACAG	TGACAGTGAT	GGGGAGGCCC	2520
TGGGCGGCAA	CCC GATGGTG	GCAGGGTTCC	AGGACGATGT	GGACCTCGAA	GACCAGCCAC	2580

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GTGGGAGTCC	CCCGCTGCCT	GCAGGCCCCG	TCCCCAGTCA	AGACATCACT	CTTTCGAGTG	2640
AGGAGGAAGC	AGAAGTGGCA	GCTCCCACAA	AAGGCCCTGC	CCCAGCTCCC	CAGCAGTGCT	2700
CAGAGCCAGA	GACCAAGTGG	TCCTCCATAC	CAGCTTCGAA	GCCACGGAGG	GGGACAGCTC	2760
CCACGAGGAC	CGCAGCACCC	CCCTGGCCAG	GCGGTGTCTC	TGTTTCGCACA	GGTCCGGAGA	2820
AGCGCAGCAG	CACCAGGCCC	CCTGCTGAGA	TGGAGCCGGG	GAAGGGTGAG	CAGGCCTCCT	2880
CGTCGGAGAG	TGACCCCGAG	GGACCCATTG	CTGCACAAAT	GCTGTCTCTT	GTCAATGGATG	2940
ACCCCGACTT	TGAGAGCGAG	GGATCAGACA	CACAGCGCAG	GGCGGATGAC	TTTCCCGTGC	3000
GAGATGACCC	CTCCGATGTG	ACTGACGAGG	ATGAGGGCCC	TGCCGAGCCG	CCCCCAGCCC	3060
CCAAGCTCCC	TCTCCCCGCC	TTCAGACTGA	AGAATGACTC	GGACCTCTTC	GGGCTGGGGC	3120
TGGAGGAGGC	CGGACCCAAG	GAGAGCAGTG	AGGAAGGTAA	GGAGGGCAAA	ACCCCTCTTA	3180
AGGAGAAGAA	AAAAAAAACA	AAAAGCTTCT	CGAGAGTACT	TCTAGAGCGG	CCGCGTGCCC	3240
ATCGATTTTC	CACCCGGGTG	GGGTACCAGG	TAAGTGATACC	CAATTGCGCC	TATAGTGAGT	3300
CGTATT						3306

- (2) INFORMATION FOR SEQ ID NO:11:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCGGGGGCCA GAGTGGGCTG 20

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAGTCCTGG CCTGCGGATG 20

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCGACAGGA GAATTGGTTC 20

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
- GTCCTAATGT TTTCAGGGAG 20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

AAAACCTATG GTTACAATTC 20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

TCCTAGACAT GGTTC AAGTG 20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

GATATAATTA GTTCTCCATC 20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(D) TOPOLOGY: linear

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(D) TOPOLOGY: linear

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(D) TOPOLOGY: linear

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(D) TOPOLOGY: linear

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(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTTCCCAGAG CTTGTCTGTG

20

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTTTGGCAGA CTCATAGTTG

20

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TAGCAGGGAG CCATGACCTG

20

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTTGCGCCA GAAGCGAGAG

20

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

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CCTCTCTCTC TCTCTCTCTC

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(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TCCCCGCTGA TTCCGCCAAG

20

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTTTTGAAT TCGGCACGAG

20

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCCCTGGTCC GCACCAGTTC

20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAGAAGGGTC GGGGCGGCAG

20

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

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(D) TOPOLOGY: linear

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(D) TOPOLOGY: linear

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(D) TOPOLOGY: linear

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(D) TOPOLOGY: linear

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GATCCTCTGA ACCTGCAGAG 20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GGAAATGAGG TGGGGCGATC 20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

CTTTGCCTTG GACAAGGATG 20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GCACCTGCCA TTGGGGGTAG 20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

TGCGTCTCTC GTCGCTGCTG

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCGGAACTC TGTGGTGCTG

20

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AGGATTGCCT TCCTCTACTG

20

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TGTCTGTTTC ACCAGGGGCAG

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(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

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CCAGTGCCTC TATGCATGTC

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(i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

AGGAAGCCCA CGCACACCAC

20

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CCCTTTGTTC CCTGATCTTC

20

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CGCTCGGGAT CCAGGTCATC

20

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

TCTTGGATCT CTGGCACCTC

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

CCATCAGAGT GAAGGAGGAG

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

CCATCTTCCA CTGGTCAGAG

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

CTCCTTCTCT TGGATCTCTG

20

(2) INFORMATION FOR SEQ ID NO:85:

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:
- TTACTTCAGC ACTGTTAGTC 20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

AGGGAGGTAG CTCAAAGCTC 20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

TGGGTCCACA GTTCGCACAG 20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

CAACTCTGTG ATGGCTCCAG 20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

AGCAGGGTTC TGTTCAAGAC

20

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CCATTGGGTG CTAGTCTCTC

20

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CAGCCATGCT GTCCCAGCAG

20

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

- CTGGACCTGA GGTAGCGCTG

20

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATAACCACCC TGAGGCACTG

20

(2) INFORMATION FOR SEQ ID NO:94:

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(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GGGTGTGGTG CAGATGAGTC

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(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

ATCACACTCT TATAGCTCAG

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GTGGGAAGCT TTCCTCAGAC

20

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

TGATGAACAT GGGCCTGGAG

20

(A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CATTGTGGAT GTACTACCAC

20

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TGTGTTTTGC AACCTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ATAGTGGCAC CACTTACGAG

20

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AATTCTGCAA CGTGATGGCG

20

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

00700354.41300  
00E1T1"45E00260

CACAAGATGC CTCGTCTGTG

20

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

AATCCGGACA AGGTACAGTC

20

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GCACGAGTGG CACAAGCGTG

20

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCAAGCGTGT GGTGTCAGTG

20

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

TGTTTGAACA GGCTCTGGAC

20

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TGAGTGAGGA GGCAGATGTC

20

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGGCTTTGAA GAAAGAGCTG

20

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GCAAAAGACC AGGCTGACTG

20

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGCAGCTCCT TGGTCTTCTC

20

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GATTCACAGT CCCAAGGCTC

20

(2) INFORMATION FOR SEQ ID NO:125:

09700354.14.300

09700354-11300

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ATCTGGATGA GGCGGTTGAG

20

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GGTCACTCTC CGACGAGGAG

20

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GGATCCAAAG TTCGTCTCTG

20

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CGCTGTGTGT CTGATCCCTC

20

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

060354 113000

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**00000000000000000000000000000000**

CGCAACAGCG TCTCCCTCTG

(2) INFORMATION FOR SEQ ID NO:139:

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

AGTACCTTCA TAAGTTCTTC

(2) INFORMATION FOR SEQ ID NO:140:

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

TCCCAGACTT CAACCTTCAC

(2) INFORMATION FOR SEQ ID NO:141:

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

AAACATCTTC CCGGTCGGAC

(2) INFORMATION FOR SEQ ID NO:142:

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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0900354-11300

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

20

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

20

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

20

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

20

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

0970354 11300

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 378...1799  
(D) OTHER INFORMATION:

GGATCCAAAG	GACGCCCCCG	CCGACAGGAG	AATTGGTTCC	CGGGCCCGCG	GCGATGCCCC	60										
CCCGGTAGCT	CGGGCCCGTG	GTCGGGTGTT	TGTGAGTGTT	TCTATGTGGG	AGAAGGAGGA	120										
GGAGGAGGAA	GAAGAAGCAA	CGATTTGTCT	TCTCGGCTGG	TCTCCCCCGG	GCTCTACATG	180										
TTCCCCGCAC	TGAGGAGACG	GAAGAGGAGC	CGTAGCCGCC	CCCCCTCCCG	GCCCGGATTA	240										
TAGTCTCTCG	CCACAGCGGC	CTCGGCCTCC	CCTTGGATTG	AGACGCCGAT	TCGCCCAGTG	300										
TTTGGGAAAT	GGAAGTAAT	GACAGCTGGC	ACCTGAACTA	AGTACTTTTA	TAGGCAACAC	360										
CATTCCAGAA	ATTCAGG	ATG	AAT	GGG	GAT	ATG	CCC	CAT	GTC	CCC	ATT	ACT	410			
		Met	Asn	Gly	Asp	Met	Pro	His	Val	Pro	Ile	Thr				
		1				5					10					
ACT	CTT	GCG	GGG	ATT	GCT	AGT	CTC	ACA	GAC	CTC	CTG	AAC	CAG	CTG	CCT	458
Thr	Leu	Ala	Gly	Ile	Ala	Ser	Leu	Thr	Asp	Leu	Leu	Asn	Gln	Leu	Pro	
			15					20					25			
CTT	CCA	TCT	CCT	TTA	CCT	GCT	ACA	ACT	ACA	AAG	AGC	CTT	CTC	TTT	AAT	506
Leu	Pro	Ser	Pro	Leu	Pro	Ala	Thr	Thr	Thr	Lys	Ser	Leu	Leu	Phe	Asn	
		30					35					40				
GCA	CGA	ATA	GCA	GAA	GAG	GTG	AAC	TGC	CTT	TTG	GCT	TGT	AGG	GAT	GAC	554
Ala	Arg	Ile	Ala	Glu	Glu	Val	Asn	Cys	Leu	Leu	Ala	Cys	Arg	Asp	Asp	
	45					50					55					
AAT	TTG	GTT	TCA	CAG	CTT	GTC	CAT	AGC	CTC	AAC	CAG	GTA	TCA	ACA	GAT	602
Asn	Leu	Val	Ser	Gln	Leu	Val	His	Ser	Leu	Asn	Gln	Val	Ser	Thr	Asp	
60					65					70					75	
CAC	ATA	GAG	TTG	AAA	GAT	AAC	CTT	GGC	AGT	GAT	GAC	CCA	GAA	GGT	GAC	650
His	Ile	Glu	Leu	Lys	Asp	Asn	Leu	Gly	Ser	Asp	Asp	Pro	Glu	Gly	Asp	
				80				85						90		
ATA	CCA	GTC	TTG	TTG	CAG	GCC	GTC	CTG	GCA	AGG	AGT	CCT	AAT	GTT	TTC	698
Ile	Pro	Val	Leu	Leu	Gln	Ala	Val	Leu	Ala	Arg	Ser	Pro	Asn	Val	Phe	
		95						100					105			
AGG	GAG	AAA	AGC	ATG	CAG	AAC	AGA	TAT	GTA	CAA	AGT	GGA	ATG	ATG	ATG	746
Arg	Glu	Lys	Ser	Met	Gln	Asn	Arg	Tyr	Val	Gln	Ser	Gly	Met	Met	Met	
		110					115					120				
TCT	CAG	TAT	AAA	CTT	TCT	CAG	AAT	TCC	ATG	CAC	AGT	AGT	CCT	GCA	TCT	794
Ser	Gln	Tyr	Lys	Leu	Ser	Gln	Asn	Ser	Met	His	Ser	Ser	Pro	Ala	Ser	
	125					130					135					
TCC	AAT	TAT	CAA	CAA	ACC	ACT	ATC	TCA	CAT	AGC	CCC	TCC	AGC	CGG	TTT	842

Ser	Asn	Tyr	Gln	Gln	Thr	Thr	Ile	Ser	His	Ser	Pro	Ser	Ser	Arg	Phe	
140					145					150					155	
GTG	CCA	CCA	CAG	ACA	AGC	TCT	GGG	AAC	AGA	TTT	ATG	CCA	CAG	CAA	AAT	890
Val	Pro	Pro	Gln	Thr	Ser	Ser	Gly	Asn	Arg	Phe	Met	Pro	Gln	Gln	Asn	
				160				165						170		
AGC	CCA	GTG	CCT	AGT	CCA	TAC	GCC	CCA	CAA	AGC	CCT	GCA	GGA	TAC	ATG	938
Ser	Pro	Val	Pro	Ser	Pro	Tyr	Ala	Pro	Gln	Ser	Pro	Ala	Gly	Tyr	Met	
			175					180					185			
CCA	TAT	TCC	CAT	CCT	TCA	AGT	TAC	ACA	ACA	CAT	CCA	CAG	ATG	CAA	CAA	986
Pro	Tyr	Ser	His	Pro	Ser	Ser	Tyr	Thr	Thr	His	Pro	Gln	Met	Gln	Gln	
	190						195					200				
GCA	TCG	GTA	TCA	AGT	CCC	ATT	GTT	GCA	GGT	GGT	TTG	AGA	AAC	ATA	CAT	1034
Ala	Ser	Val	Ser	Ser	Pro	Ile	Val	Ala	Gly	Gly	Leu	Arg	Asn	Ile	His	
	205					210					215					
GAT	AAT	AAA	GTT	TCT	GGT	CCG	TTG	TCT	GGC	AAT	TCA	GCT	AAT	CAT	CAT	1082
Asp	Asn	Lys	Val	Ser	Gly	Pro	Leu	Ser	Gly	Asn	Ser	Ala	Asn	His	His	
	220				225					230					235	
GCT	GAT	AAT	CCT	AGA	CAT	GGT	TCA	AGT	GAG	GAC	TAC	CTA	CAC	ATG	GTG	1130
Ala	Asp	Asn	Pro	Arg	His	Gly	Ser	Ser	Glu	Asp	Tyr	Leu	His	Met	Val	
				240					245					250		
CAC	AGG	CTA	AGT	AGT	GAC	GAT	GGA	GAT	TCT	TCA	ACA	ATG	AGG	AAT	GCT	1178
His	Arg	Leu	Ser	Ser	Asp	Asp	Gly	Asp	Ser	Ser	Thr	Met	Arg	Asn	Ala	
			255					260					265			
GCA	TCT	TTT	CCC	TTG	AGA	TCT	CCA	CAG	CCA	GTA	TGC	TCC	CCT	GCT	GGA	1226
Ala	Ser	Phe	Pro	Leu	Arg	Ser	Pro	Gln	Pro	Val	Cys	Ser	Pro	Ala	Gly	
	270						275				280					
AGT	GAA	GGA	ACT	CCT	AAA	GGC	TCA	AGA	CCA	CCT	TTA	ATC	CTA	CAA	TCT	1274
Ser	Glu	Gly	Thr	Pro	Lys	Gly	Ser	Arg	Pro	Pro	Leu	Ile	Leu	Gln	Ser	
	285					290					295					
CAG	TCT	CTA	CCT	TGT	TCA	TCA	CCT	CGA	GAT	GTT	CCA	CCA	GAT	ATC	TTG	1322
Gln	Ser	Leu	Pro	Cys	Ser	Ser	Pro	Arg	Asp	Val	Pro	Pro	Asp	Ile	Leu	
	300				305					310					315	
CTA	GAT	TCT	CCA	GAA	AGA	AAA	CAA	AAG	AAG	CAG	AAG	AAA	ATG	AAA	TTA	1370
Leu	Asp	Ser	Pro	Glu	Arg	Lys	Gln	Lys	Lys	Gln	Lys	Lys	Met	Lys	Leu	
				320					325				330			
GGC	AAG	GAT	GAA	AAA	GAG	CAG	AGT	GAG	AAA	GCG	GCA	ATG	TAT	GAT	ATA	1418
Gly	Lys	Asp	Glu	Lys	Glu	Gln	Ser	Glu	Lys	Ala	Ala	Met	Tyr	Asp	Ile	
			335					340				345				
ATT	AGT	TCT	CCA	TCC	AAG	GAC	TCT	ACT	AAA	CTT	ACA	TTA	AGA	CTT	TCT	1466
Ile	Ser	Ser	Pro	Ser	Lys	Asp	Ser	Thr	Lys	Leu	Thr	Leu	Arg	Leu	Ser	
	350						355					360				
CGT	GTA	AGG	TCT	TCA	GAC	ATG	GAC	CAG	CAA	GAG	GAT	ATG	ATT	TCT	GGT	1514
Arg	Val	Arg	Ser	Ser	Asp	Met	Asp	Gln	Gln	Glu	Asp	Met	Ile	Ser	Gly	

365					370					375							
GTG	GAA	AAT	AGC	AAT	GTT	TCA	GAA	AAT	GAT	ATT	CCT	TTT	AAT	GTG	CAG	1562	
Val	Glu	Asn	Ser	Asn	Val	Ser	Glu	Asn	Asp	Ile	Pro	Phe	Asn	Val	Gln		
380					385					390					395		
TAC	CCA	GGA	CAG	ACT	TCA	AAA	ACA	CCC	ATT	ACT	CCA	CAA	GAT	ATA	AAC	1610	
Tyr	Pro	Gly	Gln	Thr	Ser	Lys	Thr	Pro	Ile	Thr	Pro	Gln	Asp	Ile	Asn		
400					405					410							
CGC	CCA	CTA	AAT	GCT	GCT	CAA	TGT	TTG	TCG	CAG	CAA	GAA	CAA	ACA	GCA	1658	
Arg	Pro	Leu	Asn	Ala	Ala	Gln	Cys	Leu	Ser	Gln	Gln	Glu	Gln	Thr	Ala		
415					420					425							
TTC	CTT	CCA	GCA	AAT	CAA	GTG	CCT	GTT	TTA	CAA	CAG	AAC	ACT	TCA	GTT	1706	
Phe	Leu	Pro	Ala	Asn	Gln	Val	Pro	Val	Leu	Gln	Gln	Asn	Thr	Ser	Val		
430					435					440							
GCT	GCA	AAA	CAA	CCC	CAG	ACC	AAT	AGT	CAC	AAA	ACC	TTG	GTG	CAG	CCT	1754	
Ala	Ala	Lys	Gln	Pro	Gln	Thr	Asn	Ser	His	Lys	Thr	Leu	Val	Gln	Pro		
445					450					455							
GGA	ACA	GGC	ATA	GAG	GTC	TCA	GCA	GAG	CTG	CCC	AAG	GAC	AAG	ACC	TAAGA	1804	
Gly	Thr	Gly	Ile	Glu	Val	Ser	Ala	Glu	Leu	Pro	Lys	Asp	Lys	Thr			
460					465					470							
TCCAGCAGGG	AACTATGTAG	TCACCCCGAG	AGGCCCAGCT	CTCTCCGTGA	GCTCTGGGCC	1864											
TAGGGTGGGG	GTGGTTGTTG	GTTCTGCGCG	CACTGTTCCC	CCTACATGAT	GGGTCCATCC	1924											
CAGTTGGCTT	CTCTCACTCG	CTTCCTCCTG	TGGAGAAGCC	TGTCCAGGTG	TCACTGCCTC	1984											
CAGGAAGCTG	TCTCTGATTT	CTCCAGTTGA	ACAGTGAGAT	TTGCCACACC	TCACATGCAT	2044											
CGCTCTTGTC	CCTGGAATTG	TAACCATAGG	TTTTCTTGTC	TCCTGGAGGA	CAAGGATGAG	2104											
GGCTTTCCAC	TTGAGTCTCC	CTGGTGAGC	CCAGCTCCTG	ACATACCTGG	TAAAAGTTCT	2164											
CAAGAGAAGA	ACATGGAGGA	GGAATGTGGA	TAACAACCTT	GGCTGCCTGT	GTGTTCCAAG	2224											
CTAGGAAGAT	GTAATGTCCC	CACAAACGGG	GTAAATGGCT	TGCCTGCGTC	ACAGCTGTCT	2284											
CAAGCCCAGG	CCCTGGGCGC	CAGCCCCAAG	CCAAGGACTA	GGTCCAGAGC	CACACAGCGC	2344											
CAGGCCACAT	CCGCCTCACC	TGGGACCCCT	TGTGGGGTAC	AGTCTCCGGC	CCCACCCAGA	2404											
CCTCCTGAAG	GAGAGACCCC	ATTGGCAAGGA	CTCAGCCACC	TGCAGTTTCA	TAAGCCCCCA	2464											
CTGGGTTCCCT	AGGCATGAAG	ATCCACGGTT	AGAGGCTGAA	CTGGCAGGAA	CCTGTCTCCA	2524											
GCCCCCTTCTC	ACCCCAGCCG	GGCCCTGCCT	CAGAGGCAGC	ACCCAGGACG	TGGCCATGAC	2584											
CCGTGGACTC	CACTCAATCC	CTCTTCTCCA	GGAGCCATGC	AAAGTGTGAG	CCAGCCAGGC	2644											
CCCTGGAAGG	CAGTCATCAC	CTCTTAAGGC	ATTGTGGGTG	TCGGTCCTGC	AACTGCCAGG	2704											
TGCAGCACAC	GACCCGTGTC	CGGTGTTCTGA	TAGCAGGGAG	CCATGACCTG	GCAACGATTC	2764											
CACGCTCAAA	GGGGCACCCG	GGGGGCCCTG	GGTCGGGGCG	GATCAGCTTT	CCCTGGGCAC	2824											
ATCTGCCTCA	TTCCAGATCT	CCAGGGCTCA	TGTCTGTGAC	AGGGAGGGAA	GGCTCTGCCC	2884											
TGGCCTTCCG	TCAGTCTGTC	CAGTGCAGGC	TGGGCAGCCT	GGGCTTTAGA	GCTGGCTTCT	2944											
GCCCACACTT	TCTCCGTGAA	AGGAAAACAA	CTATGAGTCT	GCCAAACGCA	TCTCAGATGC	3004											
GTTTTAAAAA	ATTCTGGTCC	CCGCTCTCTG	TCCCATCATC	CGCCTCGGGG	ACTTCCTCTC	3064											
TCCGTGGTTC	TCACCCCATTA	CTCTGTCACT	GCCACATTTT	CACCTGGGCC	TGGCCTTTGT	3124</											

AGCCGGGGCC	TCCGCTCTCG	GGTGACCCGG	TGAGACCCCC	GGGGAGGCCG	CTGGGGAGGC	3724
GCGGGCTCTG	CTCCCGGGTC	CCAAACGCAC	TGGCTGCCCC	TCAGGAGGGA	CGGCGACCTC	3784
CACCCACGGC	GCTGGCGCCC	GCACGGCCGC	TCCTCCCGCT	CCCGCAGCCT	GGACGCCTCC	3844
CGAGGCCGCC	CCGCCGGGCC	CCACGCGCGG	CCCCATCCGC	AGGCCAGGAC	TGCCTTCCCG	3904
GAGCTGGCGG	CCCCCAGCCT	GGAGGAGCCG	GCCCCAGACG	CCCTCCCAGC	CCTCCCCAGC	3964
CCACTCTGGC	CCCGCAGCCC	CCGCCTGGTC	CGAGTGCGGG	TCTCTGGCCC	CGGCCTTTCC	4024
CGGGGAAGGA	AAGCAAAAAG	CTT				4047

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met	Asn	Gly	Asp	Met	Pro	His	Val	Pro	Ile	Thr	Thr	Leu	Ala	Gly	Ile
1				5					10					15	
Ala	Ser	Leu	Thr	Asp	Leu	Leu	Asn	Gln	Leu	Pro	Leu	Pro	Ser	Pro	Leu
			20					25					30		
Pro	Ala	Thr	Thr	Thr	Lys	Ser	Leu	Leu	Phe	Asn	Ala	Arg	Ile	Ala	Glu
			35				40					45			
Glu	Val	Asn	Cys	Leu	Leu	Ala	Cys	Arg	Asp	Asp	Asn	Leu	Val	Ser	Gln
			50			55				60					
Leu	Val	His	Ser	Leu	Asn	Gln	Val	Ser	Thr	Asp	His	Ile	Glu	Leu	Lys
65					70				75					80	
Asp	Asn	Leu	Gly	Ser	Asp	Asp	Pro	Glu	Gly	Asp	Ile	Pro	Val	Leu	Leu
			85					90						95	
Gln	Ala	Val	Leu	Ala	Arg	Ser	Pro	Asn	Val	Phe	Arg	Glu	Lys	Ser	Met
			100					105					110		
Gln	Asn	Arg	Tyr	Val	Gln	Ser	Gly	Met	Met	Met	Ser	Gln	Tyr	Lys	Leu
			115				120					125			
Ser	Gln	Asn	Ser	Met	His	Ser	Ser	Pro	Ala	Ser	Ser	Asn	Tyr	Gln	Gln
			130			135					140				
Thr	Thr	Ile	Ser	His	Ser	Pro	Ser	Ser	Arg	Phe	Val	Pro	Pro	Gln	Thr
145					150				155					160	
Ser	Ser	Gly	Asn	Arg	Phe	Met	Pro	Gln	Gln	Asn	Ser	Pro	Val	Pro	Ser
			165					170					175		
Pro	Tyr	Ala	Pro	Gln	Ser	Pro	Ala	Gly	Tyr	Met	Pro	Tyr	Ser	His	Pro
			180				185					190			
Ser	Ser	Tyr	Thr	Thr	His	Pro	Gln	Met	Gln	Gln	Ala	Ser	Val	Ser	Ser
			195			200					205				
Pro	Ile	Val	Ala	Gly	Gly	Leu	Arg	Asn	Ile	His	Asp	Asn	Lys	Val	Ser
			210			215					220				
Gly	Pro	Leu	Ser	Gly	Asn	Ser	Ala	Asn	His	His	Ala	Asp	Asn	Pro	Arg
225					230				235					240	
His	Gly	Ser	Ser	Glu	Asp	Tyr	Leu	His	Met	Val	His	Arg	Leu	Ser	Ser
			245					250					255		
Asp	Asp	Gly	Asp	Ser	Ser	Thr	Met	Arg	Asn	Ala	Ala	Ser	Phe	Pro	Leu
			260					265					270		
Arg	Ser	Pro	Gln	Pro	Val	Cys	Ser	Pro	Ala	Gly	Ser	Glu	Gly	Thr	Pro
			275				280						285		

0970034-11300



CAG	AAA	GAC	AAA	CAG	TCT	TAT	CGG	GAC	CTC	AAA	GAA	GTA	ACT	CCT	GAA		244
Gln	Lys	Asp	Lys	Gln	Ser	Tyr	Arg	Asp	Leu	Lys	Glu	Val	Thr	Pro	Glu		
		60					65					70					
GGG	CTC	CAA	ATG	GTA	AAG	AAA	AAC	TTT	GAG	TGG	GTT	GCA	GAG	AGA	GTA		292
Gly	Leu	Gln	Met	Val	Lys	Lys	Asn	Phe	Glu	Trp	Val	Ala	Glu	Arg	Val		
	75					80					85						
GAG	TTG	CTT	TTG	AAA	TCA	GAA	AGT	CAG	TGC	AGG	GTT	GTA	GTG	TTG	ATG		340
Glu	Leu	Leu	Leu	Lys	Ser	Glu	Ser	Gln	Cys	Arg	Val	Val	Val	Leu	Met		
90					95					100					105		
GGC	TCT	ACT	TCT	GAT	CTT	GGT	CAC	TGT	GAA	AAA	ATC	AAG	AAG	GCC	TGT		388
Gly	Ser	Thr	Ser	Asp	Leu	Gly	His	Cys	Glu	Lys	Ile	Lys	Lys	Ala	Cys		
				110					115					120			
GGA	AAT	TTT	GGC	ATT	CCA	TGT	GAA	CTT	CGA	GTA	ACA	TCT	GCG	CAT	AAA		436
Gly	Asn	Phe	Gly	Ile	Pro	Cys	Glu	Leu	Arg	Val	Thr	Ser	Ala	His	Lys		
			125					130					135				
GGA	CCA	GAT	GAA	ACT	CTG	AGG	ATT	AAA	GCT	GAG	TAT	GAA	GGG	GAT	GGC		484
Gly	Pro	Asp	Glu	Thr	Leu	Arg	Ile	Lys	Ala	Glu	Tyr	Glu	Gly	Asp	Gly		
		140					145					150					
ATT	CCT	ACT	GTA	TTT	GTG	GCA	GTG	GCA	GGC	AGA	AGT	AAT	GGT	TTG	GGA		532
Ile	Pro	Thr	Val	Phe	Val	Ala	Val	Ala	Gly	Arg	Ser	Asn	Gly	Leu	Gly		
	155					160						165					
CCA	GTG	ATG	TCT	GGG	AAC	ACT	GCA	TAT	CCA	GTT	ATC	AGC	TGT	CCT	CCC		580
Pro	Val	Met	Ser	Gly	Asn	Thr	Ala	Tyr	Pro	Val	Ile	Ser	Cys	Pro	Pro		
170					175					180					185		
CTC	ACA	CCA	GAC	TGG	GGA	GTT	CAG	GAT	GTG	TGG	TCT	TCT	CTT	CGA	CTA		628
Leu	Thr	Pro	Asp	Trp	Gly	Val	Gln	Asp	Val	Trp	Ser	Ser	Leu	Arg	Leu		
				190					195					200			
CCC	AGT	GGT	CTT	GGC	TGT	TCA	ACC	GTA	CTT	TCT	CCA	GAA	GGA	TCA	GCT		676
Pro	Ser	Gly	Leu	Gly	Cys	Ser	Thr	Val	Leu	Ser	Pro	Glu	Gly	Ser	Ala		
			205					210					215				
CAA	TTT	GCT	GCT	CAG	ATA	TTT	GGG	TTA	AGC	AAC	CAT	TTG	GTA	TGG	AGC		724
Gln	Phe	Ala	Ala	Gln	Ile	Phe	Gly	Leu	Ser	Asn	His	Leu	Val	Trp	Ser		
		220					225					230					
AAA	CTG	CGA	GCA	AGC	ATT	TTG	AAC	ACA	TGG	ATT	TCC	TTG	AAG	CAG	GCT		772
Lys	Leu	Arg	Ala	Ser	Ile	Leu	Asn	Thr	Trp	Ile	Ser	Leu	Lys	Gln	Ala		
	235					240					245						
GAC	AAG	AAA	ATC	AGA	GAA	TGT	AAT	TTA	TAAGAAAGAA	TGCCATTGAA	TTTTTTTA						826
Asp	Lys	Lys	Ile	Arg	Glu	Cys	Asn	Leu									
250					255												



CCAGGGGAGT	CCGAGAAGAG	CTGCCATTGG	CTGACAGGGC	ATTTTCAGGC	TCTGTCATTG	1126
GTCAGGGAGC	ACACCCCAGC	CTGAAGAGTG	ATGCCATTGG	CCAGGGAGTG	GTTTTGTCAT	1186
AGCCGTTGGC	TGTGAAGTGG	AAGGAAAAGA	TCTGGGAATG	AAGCCCTGTG	GCCAGGAAGA	1246
TAGACAGGGC	AGCAACTTCT	GGGCCTCCAG	GCCCTCTTCC	CACCATAGCA	ATGTGGGCAA	1306
AACTGGTGTC	AGGCCCCAGC	CAGAAAAAGG	AGCCCAAGCC	AGAGGGCAAG	TGACAAAAGGA	1366
TGTACCATGT	CCAATCTCCC	ACACCCTGGG	GCTGCCCTTC	CCAATGTCTT	TCTTGATAGC	1426
CAAGTTGGGC	TGGGAGCAGC	TCACTGCTCC	TCTAGCCAGG	AGGGTTTCTC	AGCTCCTGGA	1486
GGCCGCAGCT	TGATGTTGAA	CTGCTGCAGG	GTCTGCTCCA	GCTGTTTCTG	GTTCCAGCA	1546
AAGTAGGCGG	ACACAGCATT	GTGGAAGAGC	AGCAGCTGCT	TGTGCATCAC	CTTGATCTTG	1606
TTTTCTTCCA	GGAAC TTGAG	CTTGATGGCC	ACATCTCCCC	GCAGCTTCTC	ATACTTGTC	1666
CGATGGGCCT	GGAAAGTGGC	CTGGGCACTC	TCAAGTCGAC	CACGTGTCCC	TGCATCCCGG	1726
GGGCCTAGAC	TCAGCTCCTC	TAAGTCTGTT	CGGTAGGCAT	CATATTCCAG	CCTGGCAGCC	1786
TCATACTGTT	TCACAGTCAT	GAGCGTGTCT	TCCATGGTCT	TGGTGACCAA	TGTGTTGATG	1846
CTAGAGACAA	AGAAGTTCAC	GGCTCCTAGC	AGCGTTTCCC	CATTCTTGCA	TAGTAGTTTC	1906
TGTGTCTCTG	CATTGTAGCC	AAATTCCTCC	TGAAGCTCTG	GGGACTTCTG	GCTGAGGTCA	1966
GCAAAGGCAT	CACCCAGTGC	ATGCTGGGTC	TGCAGCAGGC	TGTAGAGGTG	GGCTGTCACT	2026
GCCCGGCCCA	GCTGCAGGAC	ACTCTCATAC	TTGCGCTTCG	TCTCACGCAG	CAACTCAATC	2086
TGCAGCTCTA	GCTCCAGGAT	TCCGGCGCCT	CCACTCCGTC	CCCCGCGGGT	CTGCTCTGTG	2146
TGCCATGGAC	GGCATTGTCC	CAGATATAGC	CGTTGGTACA	AAGCGGGGAT	CTGACGAGCT	2206
TTTCTCTACT	TGTGTCACTA	ACGGACCGTT	TATCATGAGC	AGCAACTCGG	CTTCTGCAGC	2266
AAACGGAAAT	GACAGCAAGA	AGTTCAAAGG	TGACAGCCGA	AGTGCAGGCG	TCCCCTCTAG	2326
AGTGATCCAC	ATCCGGAAGC	TCCCCATCGA	CGTCACGGAG	GGGGAAGTCA	TCTCCCTGGG	2386
GCTGCCCTTT	GGGAAGGTCA	CCAACCTCCT	GATGCTGAAG	GGGAAAAACC	AGGCCTTCAT	2446
CGAGATGAAC	ACGGAGGAGG	CTGCCAATAC	CATGGTGAAC	TACTACACCT	CGGTGACCCC	2506
TGTGCTGCGC	GGCCAGCCCA	TCTACATCCA	GTTCTCCAAC	CACAAGGAGC	TGAAGACCGA	2566
CAGCTCTCCC	AACCAGGCGC	GGGCCCAGGC	GGCCCTGCAG	GCGGTGAACT	CGGTCCAGTC	2626
GGGGAACCTG	GCCTTGGCTG	CCTCGGCGGC	GGCCGTGGAT	GCAGGGATGG	CGATGGCCGG	2686
GCAGAGCCCC	GTGCTCAGGA	TCATCGTGGA	GAACCTCTTC	TACCCTGTGA	CCCTGGATGT	2746
GCTGCACCAG	ATTTTCTCCA	AGTTCGGCAC	AGTGTGGAAG	ATCATCACCT	TCACCAAGAA	2806
CAACCAGTTC	CAGGCCCTGC	TGCAGTATGC	GGACCCCGTG	AGCGCCCAGC	ACGCCAAGCT	2866
GTCGCTGGAC	GGGCAGAACA	TCTACAACGC	CTGCTGCACG	CTGCGCATCG	ACTTTTCCAA	2926
GCTCACCAGC	CTCAACGTCA	AGTACAACAA	TGACAAGAGC	CGTGACTACC	TCGTGCCGAA	2986
TTCTTTGGAT	CC					2998

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Ala	Thr	Gln	Ala	Ile	Phe	Glu	Ile	Leu	Glu	Lys	Ser	Trp	Leu	Pro	Gln
1			5					10					15		
Asn	Cys	Thr	Leu	Val	Asp	Met	Lys	Ile	Glu	Phe	Gly	Val	Asp	Val	Thr
			20					25					30		
Thr	Lys	Glu	Ile	Val	Leu	Ala	Asp	Val	Ile	Asp	Asn	Asp	Ser	Trp	Arg
			35					40					45		
Leu	Trp	Pro	Ser	Gly	Asp	Arg	Ser	Gln	Gln	Lys	Asp	Lys	Gln	Ser	Tyr
			50					55					60		
Arg	Asp	Leu	Lys	Glu	Val	Thr	Pro	Glu	Gly	Leu	Gln	Met	Val	Lys	Lys
65						70				75					80

Asn	Phe	Glu	Trp	Val	Ala	Glu	Arg	Val	Glu	Leu	Leu	Leu	Lys	Ser	Glu	
				85					90					95		
Ser	Gln	Cys	Arg	Val	Val	Val	Leu	Met	Gly	Ser	Thr	Ser	Asp	Leu	Gly	
			100					105					110			
His	Cys	Glu	Lys	Ile	Lys	Lys	Ala	Cys	Gly	Asn	Phe	Gly	Ile	Pro	Cys	
		115					120					125				
Glu	Leu	Arg	Val	Thr	Ser	Ala	His	Lys	Gly	Pro	Asp	Glu	Thr	Leu	Arg	
	130					135					140					
Ile	Lys	Ala	Glu	Tyr	Glu	Gly	Asp	Gly	Ile	Pro	Thr	Val	Phe	Val	Ala	
145					150					155					160	
Val	Ala	Gly	Arg	Ser	Asn	Gly	Leu	Gly	Pro	Val	Met	Ser	Gly	Asn	Thr	
			165					170						175		
Ala	Tyr	Pro	Val	Ile	Ser	Cys	Pro	Pro	Leu	Thr	Pro	Asp	Trp	Gly	Val	
		180						185					190			
Gln	Asp	Val	Trp	Ser	Ser	Leu	Arg	Leu	Pro	Ser	Gly	Leu	Gly	Cys	Ser	
	195					200						205				
Thr	Val	Leu	Ser	Pro	Glu	Gly	Ser	Ala	Gln	Phe	Ala	Ala	Gln	Ile	Phe	
	210					215					220					
Gly	Leu	Ser	Asn	His	Leu	Val	Trp	Ser	Lys	Leu	Arg	Ala	Ser	Ile	Leu	
225					230					235					240	
Asn	Thr	Trp	Ile	Ser	Leu	Lys	Gln	Ala	Asp	Lys	Lys	Ile	Arg	Glu	Cys	
			245					250						255		
Asn	Leu															

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1038 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Ile	Gln	Arg	Phe	Gly	Thr	Ser	Gly	His	Ile	Met	Asn	Leu	Gln	Ala	Gln	
1				5				10					15			
Pro	Lys	Ala	Gln	Asn	Lys	Arg	Lys	Arg	Cys	Leu	Phe	Gly	Gly	Gln	Glu	
		20					25					30				
Pro	Ala	Pro	Lys	Glu	Gln	Pro	Pro	Pro	Leu	Gln	Pro	Pro	Gln	Gln	Ser	
		35				40					45					
Ile	Arg	Val	Lys	Glu	Glu	Gln	Tyr	Leu	Gly	His	Glu	Gly	Pro	Gly	Gly	
50						55				60						
Ala	Val	Ser	Thr	Ser	Gln	Pro	Val	Glu	Leu	Pro	Pro	Pro	Ser	Ser	Leu	
65					70				75						80	
Ala	Leu	Leu	Asn	Ser	Val	Val	Tyr	Gly	Pro	Glu	Arg	Thr	Ser	Ala	Ala	
			85					90					95			
Met	Leu	Ser	Gln	Gln	Val	Ala	Ser	Val	Lys	Trp	Pro	Asn	Ser	Val	Met	
		100					105					110				
Ala	Pro	Gly	Arg	Gly	Pro	Glu	Arg	Gly	Gly	Gly	Gly	Gly	Val	Ser	Asp	
		115				120					125					
Ser	Ser	Trp	Gln	Gln	Gln	Pro	Gly	Gln	Pro	Pro	Pro	His	Ser	Thr	Trp	
	130					135					140					
Asn	Cys	His	Ser	Leu	Ser	Leu	Tyr	Ser	Ala	Thr	Lys	Gly	Ser	Pro	His	
145				150					155					160		
Pro	Gly	Val	Gly	Val	Pro	Thr	Tyr	Tyr	Asn	His	Pro	Glu	Ala	Leu	Lys	

															165			170			175		
Arg	Glu	Lys	Ala	Gly	Gly	Pro	Gln	Leu	Asp	Arg	Tyr	Val	Arg	Pro	Met								
															180			185			190		
Met	Pro	Gln	Lys	Val	Gln	Leu	Glu	Val	Gly	Arg	Pro	Gln	Ala	Pro	Leu								
															195			200			205		
Asn	Ser	Phe	His	Ala	Ala	Lys	Lys	Pro	Pro	Asn	Gln	Ser	Leu	Pro	Leu								
															210			215			220		
Gln	Pro	Phe	Gln	Leu	Ala	Phe	Gly	His	Gln	Val	Asn	Arg	Gln	Val	Phe								
															225			230			235		
Arg	Gln	Gly	Pro	Pro	Pro	Pro	Asn	Pro	Val	Ala	Ala	Phe	Pro	Pro	Gln								
															245			250			255		
Lys	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln								
															260			265			270		
Ala	Ala	Leu	Pro	Gln	Met	Pro	Leu	Phe	Glu	Asn	Phe	Tyr	Ser	Met	Pro								
															275			280			285		
Gln	Gln	Pro	Ser	Gln	Gln	Pro	Gln	Asp	Phe	Gly	Leu	Gln	Pro	Ala	Gly								
															290			295			300		
Pro	Leu	Gly	Gln	Ser	His	Leu	Ala	His	His	Ser	Met	Ala	Pro	Tyr	Pro								
															305			310			315		
Phe	Pro	Pro	Asn	Pro	Asp	Met	Asn	Pro	Glu	Leu	Arg	Lys	Ala	Leu	Leu								
															325			330			335		
Gln	Asp	Ser	Ala	Pro	Gln	Pro	Ala	Leu	Pro	Gln	Val	Gln	Ile	Pro	Phe								
															340			345			350		
Pro	Arg	Arg	Ser	Arg	Arg	Leu	Ser	Lys	Glu	Gly	Ile	Leu	Pro	Pro	Ser								
															355			360			365		
Ala	Leu	Asp	Gly	Ala	Gly	Thr	Gln	Pro	Gly	Gln	Glu	Ala	Thr	Gly	Asn								
															370			375			380		
Leu	Phe	Leu	His	His	Trp	Pro	Leu	Gln	Gln	Pro	Pro	Pro	Gly	Ser	Leu								
															385			390			395		
Gly	Gln	Pro	His	Pro	Glu	Ala	Leu	Gly	Phe	Pro	Leu	Glu	Leu	Arg	Glu								
															405			410			415		
Ser	Gln	Leu	Leu	Pro	Asp	Gly	Glu	Arg	Leu	Ala	Pro	Asn	Gly	Arg	Glu								
															420			425			430		
Arg	Glu	Ala	Pro	Ala	Met	Gly	Ser	Glu	Glu	Gly	Met	Arg	Ala	Val	Ser								
															435			440			445		
Thr	Gly	Asp	Cys	Gly	Gln	Val	Leu	Arg	Gly	Gly	Val	Ile	Gln	Ser	Thr								
															450			455			460		
Arg	Arg	Arg	Arg	Arg	Ala	Ser	Gln	Glu	Ala	Asn	Leu	Leu	Thr	Leu	Ala								
															465			470			475		
Gln	Lys	Ala	Val	Glu	Leu	Ala	Ser	Leu	Gln	Asn	Ala	Lys	Asp	Gly	Ser								
															485			490			495		
Gly	Ser	Glu	Glu	Lys	Arg	Lys	Ser	Val	Leu	Ala	Ser	Thr	Thr	Lys	Cys								
															500			505			510		
Gly	Val	Glu	Phe	Ser	Glu	Pro	Ser	Leu	Ala	Thr	Lys	Arg	Ala	Arg	Glu								
															515			520			525		
Asp	Ser	Gly	Met	Val	Pro	Leu	Ile	Ile	Pro	Val	Ser	Val	Pro	Val	Arg								
															530			535			540		
Thr	Val	Asp	Pro	Thr	Glu	Ala	Ala	Gln	Ala	Gly	Gly	Leu	Asp	Glu	Asp								
															545			550			555		
Gly	Lys	Gly	Leu	Glu	Gln	Asn	Pro	Ala	Glu	His	Lys	Pro	Ser	Val	Ile								
															565			570			575		
Val	Thr	Arg	Arg	Arg	Ser	Thr	Arg	Ile	Pro	Gly	Thr	Asp	Ala	Gln	Ala								
															580			585			59		

Ala	Gly	Thr	Phe	Ile	Ala	Pro	Pro	Val	Tyr	Ser	Asn	Ile	Thr	Pro	Tyr
625					630					635					640
Gln	Ser	His	Leu	Arg	Ser	Pro	Val	Arg	Leu	Ala	Asp	His	Pro	Ser	Glu
				645					650					655	
Arg	Ser	Phe	Glu	Leu	Pro	Pro	Tyr	Thr	Pro	Pro	Pro	Ile	Leu	Ser	Pro
			660					665					670		
Val	Arg	Glu	Gly	Ser	Gly	Leu	Tyr	Phe	Asn	Ala	Ile	Ile	Ser	Thr	Ser
		675					680					685			
Thr	Ile	Pro	Ala	Pro	Pro	Pro	Ile	Thr	Pro	Lys	Ser	Ala	His	Arg	Thr
	690					695					700				
Leu	Leu	Arg	Thr	Asn	Ser	Ala	Glu	Val	Thr	Pro	Pro	Val	Leu	Ser	Val
705					710					715					720
Met	Gly	Glu	Ala	Thr	Pro	Val	Ser	Ile	Glu	Pro	Arg	Ile	Asn	Val	Gly
				725					730					735	
Ser	Arg	Phe	Gln	Ala	Glu	Ile	Pro	Leu	Met	Arg	Asp	Arg	Ala	Leu	Ala
			740					745					750		
Ala	Ala	Asp	Pro	His	Lys	Ala	Asp	Leu	Val	Trp	Gln	Pro	Trp	Glu	Asp
		755					760					765			
Leu	Glu	Ser	Ser	Arg	Glu	Lys	Gln	Arg	Gln	Val	Glu	Asp	Leu	Leu	Thr
	770					775					780				
Ala	Ala	Cys	Ser	Ser	Ile	Phe	Pro	Gly	Ala	Gly	Thr	Asn	Gln	Glu	Leu
785					790					795					800
Ala	Leu	His	Cys	Leu	His	Glu	Ser	Arg	Gly	Asp	Ile	Leu	Glu	Thr	Leu
				805					810					815	
Asn	Lys	Leu	Leu	Leu	Lys	Lys	Pro	Leu	Arg	Pro	His	Asn	His	Pro	Leu
			820					825					830		
Ala	Thr	Tyr	His	Tyr	Thr	Gly	Ser	Asp	Gln	Trp	Lys	Met	Ala	Glu	Arg
		835					840					845			
Lys	Leu	Phe	Asn	Lys	Gly	Ile	Ala	Ile	Tyr	Lys	Lys	Asp	Phe	Phe	Leu
	850				855						860				
Val	Gln	Lys	Leu	Ile	Gln	Thr	Lys	Thr	Val	Ala	Gln	Cys	Val	Glu	Phe
865					870					875					880
Tyr	Tyr	Thr	Tyr	Lys	Lys	Gln	Val	Lys	Ile	Gly	Arg	Asn	Gly	Thr	Leu
				885					890					895	
Thr	Phe	Gly	Asp	Val	Asp	Thr	Ser	Asp	Glu	Lys	Ser	Ala	Gln	Glu	Glu
			900					905					910		
Val	Glu	Val	Asp	Ile	Lys	Thr	Ser	Gln	Lys	Phe	Pro	Arg	Val	Pro	Leu
		915					920					925			
Pro	Arg	Arg	Glu	Ser	Pro	Ser	Glu	Glu	Arg	Leu	Glu	Pro	Lys	Arg	Glu
						935					940				
Val	Lys	Glu	Pro	Arg	Lys	Glu	Gly	Glu	Glu	Glu	Val	Pro	Glu	Ile	Gln
945					950					955					960
Glu	Lys	Glu	Glu	Gln	Glu	Glu	Gly	Arg	Glu	Arg	Ser	Arg	Arg	Ala	Ala
				965					970					975	
Ala	Val	Lys	Ala	Thr	Gln</										

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 849 amino acids

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Ile	Arg	His	Glu	Val	Ser	Phe	Leu	Trp	Asn	Thr	Glu	Ala	Ala	Cys	Pro
1				5					10					15	
Ile	Gln	Thr	Thr	Thr	Asp	Thr	Asp	Gln	Ala	Cys	Ser	Ile	Arg	Asp	Pro
			20					25					30		
Asn	Ser	Gly	Phe	Val	Phe	Asn	Leu	Asn	Pro	Leu	Asn	Ser	Ser	Gln	Gly
		35					40					45			
Tyr	Asn	Val	Ser	Gly	Ile	Gly	Lys	Ile	Phe	Met	Phe	Asn	Val	Cys	Gly
	50					55					60				
Thr	Met	Pro	Val	Cys	Gly	Thr	Ile	Leu	Gly	Lys	Pro	Ala	Ser	Gly	Cys
65						70				75					80
Glu	Ala	Glu	Thr	Gln	Thr	Glu	Glu	Leu	Lys	Asn	Trp	Lys	Pro	Ala	Arg
				85					90					95	
Pro	Val	Gly	Ile	Glu	Lys	Ser	Leu	Gln	Leu	Ser	Thr	Glu	Gly	Phe	Ile
			100					105					110		
Thr	Leu	Thr	Tyr	Lys	Gly	Pro	Leu	Ser	Ala	Lys	Gly	Thr	Ala	Asp	Ala
		115					120					125			
Phe	Ile	Val	Arg	Phe	Val	Cys	Asn	Asp	Asp	Val	Tyr	Ser	Gly	Pro	Leu
	130					135					140				
Lys	Phe	Leu	His	Gln	Asp	Ile	Asp	Ser	Gly	Gln	Gly	Ile	Arg	Asn	Thr
145					150					155					160
Tyr	Phe	Glu	Phe	Glu	Thr	Ala	Leu	Ala	Cys	Val	Pro	Ser	Pro	Val	Asp
				165					170					175	
Cys	Gln	Val	Thr	Asp	Leu	Ala	Gly	Asn	Glu	Tyr	Asp	Leu	Thr	Gly	Leu
			180					185					190		
Ser	Thr	Val	Arg	Lys	Pro	Trp	Thr	Ala	Val	Asp	Thr	Ser	Val	Asp	Gly
		195					200					205			
Arg	Lys	Arg	Thr	Phe	Tyr	Leu	Ser	Val	Cys	Asn	Pro	Leu	Pro	Tyr	Ile
	210					215					220				
Pro	Gly	Cys	Gln	Gly	Ser	Ala	Val	Gly	Ser	Cys	Leu	Val	Ser	Glu	Gly
225					230					235					240
Asn	Ser	Trp	Asn	Leu	Gly	Val	Val	Gln	Met	Ser	Pro	Gln	Ala	Ala	Ala
				245					250					255	
Asn	Gly	Ser	Leu	Ser	Ile	Met	Tyr	Val	Asn	Gly	Asp	Lys	Cys	Gly	Asn
			260					265					270		
Gln	Arg	Phe	Ser	Thr	Arg	Ile	Thr	Phe	Glu	Cys	Ala	Gln	Ile	Ser	Gly
		275					280					285			
Ser	Pro	Ala	Phe	Gln	Leu	Gln	Asp	Gly	Cys	Glu	Tyr	Val	Phe	Ile	Trp
	290					295					300				
Arg	Thr	Val	Glu	Ala	Cys	Pro	Val	Val	Arg	Val	Glu	Gly	Asp	Asn	Cys
305					310					315					320
Glu	Val	Lys	Asp	Pro	Arg	His	Gly	Asn	Leu	Tyr	Asp	Leu	Lys	Pro	Leu
				325					330					335	
Gly	Leu	Asn	Asp	Thr	Ile	Val	Ser	Ala	Gly	Glu	Tyr	Thr	Tyr	Tyr	Phe
			340					345					350		
Arg	Val	Cys	Gly	Lys	Leu	Ser	Ser	Asp	Val	Cys	Pro	Thr	Ser	Asp	Lys
		355						360				365			
Ser	Lys	Val	Val	Ser	Ser	Cys	Gln	Glu	Lys	Arg	Glu	Pro	Gln	Gly	Phe
	370					375					380				
His	Lys	Val	Ala	Gly	Leu	Leu	Thr	Gln	Lys	Leu	Thr	Tyr	Glu	Asn	Gly
385					390					395					400

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Leu	Leu	Lys	Met	Asn	Phe	Thr	Gly	Gly	Asp	Thr	Cys	His	Lys	Val	Tyr	
				405					410					415		
Gln	Arg	Ser	Thr	Ala	Ile	Phe	Phe	Tyr	Cys	Asp	Arg	Gly	Thr	Gln	Arg	
			420					425					430			
Pro	Val	Phe	Leu	Lys	Glu	Thr	Ser	Asp	Cys	Ser	Tyr	Leu	Phe	Glu	Trp	
		435					440					445				
Arg	Thr	Gln	Tyr	Ala	Cys	Pro	Pro	Phe	Asp	Leu	Thr	Glu	Cys	Ser	Phe	
	450					455					460					
Lys	Asp	Gly	Ala	Gly	Asn	Ser	Phe	Asp	Leu	Ser	Ser	Leu	Ser	Arg	Tyr	
465					470					475					480	
Ser	Asp	Asn	Trp	Glu	Ala	Ile	Thr	Gly	Thr	Gly	Asp	Pro	Glu	His	Tyr	
				485					490					495		
Leu	Ile	Asn	Val	Cys	Lys	Ser	Leu	Ala	Pro	Gln	Ala	Gly	Thr	Glu	Pro	
			500					505					510			
Cys	Pro	Pro	Glu	Ala	Ala	Ala	Cys	Leu	Leu	Gly	Gly	Ser	Lys	Pro	Val	
		515					520					525				
Asn	Leu	Gly	Arg	Val	Arg	Asp	Gly	Pro	Gln	Trp	Arg	Asp	Gly	Ile	Ile	
	530					535					540					
Val	Leu	Lys	Tyr	Val	Asp	Gly	Asp	Leu	Cys	Pro	Asp	Gly	Ile	Arg	Lys	
545					550					555					560	
Lys	Ser	Thr	Thr	Ile	Arg	Phe	Thr	Cys	Ser	Glu	Ser	Gln	Val	Asn	Ser	
				565					570					575		
Arg	Pro	Met	Phe	Ile	Ser	Ala	Val	Glu	Asp	Cys	Glu	Tyr	Thr	Phe	Ala	
			580					585					590			
Trp	Pro	Thr	Ala	Thr	Ala	Cys	Pro	Met	Lys	Ser	Asn	Glu	His	Asp	Asp	
		595					600					605				
Cys	Gln	Val	Thr	Asn	Pro	Ser	Thr	Gly	His	Leu	Phe	Asp	Leu	Ser	Ser	
	610					615					620					
Leu	Ser	Gly	Arg	Ala	Gly	Phe	Thr	Ala	Ala	Tyr	Ser	Glu	Lys	Gly	Leu	
625					630					635					640	
Val	Tyr	Met	Ser	Ile	Cys	Gly	Glu	Asn	Glu	Asn	Cys	Pro	Pro	Gly	Val	
				645					650					655		
Gly	Ala	Cys	Phe	Gly	Gln	Thr	Arg	Ile	Ser	Val	Gly	Lys	Ala	Asn	Lys	
			660					665					670			
Arg	Leu	Arg	Tyr	Val	Asp	Gln	Val	Leu	Gln	Leu	Val	Tyr	Lys	Asp	Gly	
		675				680						685				
Ser	Pro	Cys	Pro	Ser	Lys	Ser	Gly	Leu	Ser	Tyr	Lys	Ser	Val	Ile	Ser	
		690				695					700					
Phe	Val	Cys	Arg	Pro	Glu	Ala	Gly	Pro	Thr	Asn	Arg	Pro	Met	Leu	Ile	
705					710					715					720	
Ser	Leu	Asp	Lys	Gln	Thr	Cys	Thr	Leu	Phe	Phe	Ser	Trp	His	Thr	Pro	
				725					730					735		
Leu	Ala	Cys	Glu	Gln	Ala	Thr	Glu	Cys	Ser	Val	Arg	Asn	Gly	Ser	Ser	
			740					745					750			
Ile	Val	Asp	Leu	Ser	Pro	Leu	Ile	His	Arg	Thr	Gly	Gly	Tyr	Glu	Ala	
		755				760						765				
Tyr	Asp	Glu	Ser	Glu	Asp	Asp	Ala	Ser	Asp	Thr	Asn	Pro	Asp	Phe	Tyr	
	770					775					780					
Ile	Asn	Ile	Cys	Gln	Pro	Leu	Asn	Pro	Met	His	Gly	Val	Pro	Cys	Pro	
785					790					795					800	
Ala	Gly	Ala	Ala	Val	Cys	Lys	Val	Pro	Ile	Asp	Gly	Pro	Pro	Ile	Asp	
				805					810					815		
Ile	Gly	Arg	Val	Ala	Gly	Pro	Pro	Ile	Leu	Asn	Pro	Ile	Ala	Asn	Glu	
			820					825					830			
Ile	Tyr	Leu	Asn	Phe	Glu	Ser	Ser	Thr	Pro	Cys	Gln	Glu	Phe	Ser	Cys	
		835					840					845				
Lys																

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(A) LENGTH: 852 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

Met 1	Ala	Arg	Leu	Ser 5	Arg	Pro	Glu	Arg	Pro 10	Asp	Leu	Val	Phe	Glu 15	Glu
Glu	Asp	Leu	Pro	Tyr	Glu	Glu	Glu	Ile	Met	Arg	Asn	Gln	Phe	Ser	Val
Lys	Cys	Trp	Leu	His	Tyr	Ile	Glu	Phe	Lys	Gln	Gly	Ala	Pro	Lys	Pro
Arg	Leu	Asn	Gln	Leu	Tyr	Glu	Arg	Ala	Leu	Lys	Leu	Leu	Pro	Cys	Ser
Tyr	Lys	Leu	Trp	Tyr	Arg	Tyr	Leu	Lys	Ala	Arg	Arg	Ala	Gln	Val	Lys
His	Arg	Cys	Val	Thr	Asp	Pro	Ala	Tyr	Glu	Asp	Val	Asn	Asn	Cys	His
Glu	Arg	Ala	Phe	Val	Phe	Met	His	Lys	Met	Pro	Arg	Leu	Trp	Leu	Asp
Tyr	Cys	Gln	Phe	Leu	Met	Asp	Gln	Gly	Arg	Val	Thr	His	Thr	Arg	Arg
Thr	Phe	Asp	Arg	Ala	Leu	Arg	Ala	Leu	Pro	Ile	Thr	Gln	His	Ser	Arg
Ile	Trp	Pro	Leu	Tyr	Leu	Arg	Phe	Leu	Arg	Ser	His	Pro	Leu	Pro	Glu
Thr	Ala	Val	Arg	Gly	Tyr	Arg	Arg	Phe	Leu	Lys	Leu	Ser	Pro	Glu	Ser
Ala	Glu	Glu	Tyr	Ile	Glu	Tyr	Leu	Lys	Ser	Ser	Asp	Arg	Leu	Asp	Glu
Ala	Ala	Gln	Arg	Leu	Ala	Thr	Val	Val	Asn	Asp	Glu	Arg	Phe	Val	Ser
Lys	Ala	Gly	Lys	Ser	Asn	Tyr	Gln	Leu	Trp	His	Glu	Leu	Cys	Asp	Leu
Ile	Ser	Gln	Asn	Pro	Asp	Lys	Val	Gln	Ser	Leu	Asn	Val	Asp	Ala	Ile
Ile	Arg	Gly	Gly	Leu	Thr	Arg	Phe	Thr	Asp	Gln	Leu	Gly	Lys	Leu	Trp
Cys	Ser	Leu	Ala	Asp	Tyr	Tyr	Ile	Arg	Ser	Gly	His	Phe	Glu	Lys	Ala
Arg	Asp	Val	Tyr	Glu	Glu	Ala	Ile	Arg	Thr	Val	Met	Thr	Val	Arg	Asp
Phe	Thr	Gln	Val	Phe	Asp	Ser	Tyr	Ala	Gln	Phe	Glu	Glu	Ser	Met	Ile
Ala	Ala	Lys	Met	Glu	Thr	Ala	Ser	Glu	Leu	Gly	Arg	Glu	Glu	Glu	Asp
Asp	Val	Asp	Leu	Glu	Leu	Arg	Leu	Ala	Arg	Phe	Glu	Gln	Leu	Ile	Ser
Arg	Arg	Pro	Leu	Leu	Asn	Ser	Val	Leu	Leu	Arg	Gln	Asn	Pro	His	

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His	Val	His	Glu	Trp	His	Lys	Arg	Val	Ala	Leu	His	Gln	Gly	Arg	Pro
	355						360					365			
Arg	Glu	Ile	Ile	Asn	Thr	Tyr	Thr	Glu	Ala	Val	Gln	Thr	Val	Asp	Pro
	370					375					380				
Phe	Lys	Ala	Thr	Gly	Lys	Pro	His	Thr	Leu	Trp	Val	Ala	Phe	Ala	Lys
385					390					395					400
Phe	Tyr	Glu	Asp	Asn	Gly	Gln	Leu	Asp	Asp	Ala	Arg	Val	Ile	Leu	Glu
				405					410					415	
Lys	Ala	Thr	Lys	Val	Asn	Phe	Lys	Gln	Val	Asp	Asp	Leu	Ala	Ser	Val
			420					425					430		
Trp	Cys	Gln	Cys	Gly	Glu	Leu	Glu	Leu	Arg	His	Glu	Asn	Tyr	Asp	Glu
	435						440					445			
Ala	Leu	Arg	Leu	Leu	Arg	Lys	Ala	Thr	Ala	Leu	Pro	Ala	Arg	Arg	Ala
	450					455					460				
Glu	Tyr	Phe	Asp	Gly	Ser	Glu	Pro	Val	Gln	Asn	Arg	Val	Tyr	Lys	Ser
465					470					475					480
Leu	Lys	Val	Trp	Ser	Met	Leu	Ala	Asp	Leu	Glu	Glu	Ser	Leu	Gly	Thr
				485					490					495	
Phe	Gln	Ser	Thr	Lys	Ala	Val	Tyr	Asp	Arg	Ile	Leu	Asp	Leu	Arg	Ile
			500					505					510		
Ala	Thr	Pro	Gln	Ile	Val	Ile	Asn	Tyr	Ala	Met	Phe	Leu	Glu	Glu	His
			515				520						525		
Lys	Tyr	Phe	Glu	Glu	Ser	Phe	Lys	Ala	Tyr	Glu	Arg	Gly	Ile	Ser	Leu
	530					535					540				
Phe	Lys	Trp	Pro	Asn	Val	Ser	Asp	Ile	Trp	Ser	Thr	Tyr	Leu	Thr	Lys
545					550					555					560
Phe	Ile	Ala	Arg	Tyr	Gly	Gly	Arg	Lys	Leu	Glu	Arg	Ala	Arg	Asp	Leu
				565				570						575	
Phe	Glu	Gln	Ala	Leu	Asp	Gly	Cys	Pro	Pro	Lys	Tyr	Ala	Lys	Thr	Leu
			580					585					590		
Tyr	Leu	Leu	Tyr	Ala	Gln	Leu	Glu	Glu	Glu	Trp	Gly	Leu	Ala	Arg	His
	595					600						605			
Ala	Met	Ala	Val	Tyr	Glu	Arg	Ala	Thr	Arg	Ala	Val	Glu	Pro	Ala	Gln
	610					615					620				
Gln	Tyr	Asp	Met	Phe	Asn	Ile	Tyr	Ile	Lys	Arg	Ala	Ala	Glu	Ile	Tyr
625					630					635					640
Gly	Val	Thr	His	Thr	Arg	Gly	Ile	Tyr	Gln	Lys	Ala	Ile	Glu	Val	Leu
				645					650					655	
Ser	Asp	Glu	His	Ala	Arg	Glu	Met	Cys	Leu	Arg	Phe	Ala	Asp	Met	Glu
			660					665					670		
Cys	Lys	Leu	Gly	Glu	Ile	Asp	Arg	Ala	Arg	Ala	Ile	Tyr	Ser	Phe	Cys
	675						680					685			
Ser	Gln	Ile	Cys	Asp	Pro	Arg	Thr	Thr	Gly	Ala	Phe	Trp	Gln	Thr	Trp
	690					695					700				
Lys	Asp	Phe	Glu	Val	Arg	His	Gly	Asn	Glu	Asp	Thr	Ile	Lys	Glu	Met
705					710					715					720
Leu	Arg	Ile	Arg	Arg	Ser	Val	Gln	Ala	Thr	Tyr	Asn	Thr	Gln	Val	Asn
				725				730						735	
Phe	Met	Ala	Ser	Gln	Met	Leu	Lys	Val	Ser	Gly	Ser	Ala	Thr	Gly	Thr
			740					745					750		
Val	Ser	Asp	Leu	Ala	Pro	Gly	Gln	Ser	Gly	Met	Asp	Asp	Met	Lys	Leu
	755						760					765			
Leu	Glu	Gln	Arg	Ala	Glu	Gln	Leu	Ala	Ala	Glu	Ala	Glu	Arg	Asp	Gln
	770					775					780				
Pro	Leu	Arg	Ala	Gln	Ser	Lys	Ile	Leu	Phe	Val	Arg	Ser	Asp	Ala	Ser
785					790					795					800
Arg	Glu	Glu	Leu	Ala	Glu	Leu	Ala	Gln	Gln	Val	Asn	Pro	Glu	Glu	Ile



				805					810					815			
Gln	Leu	Gly	Glu	Asp	Glu	Asp	Glu	Asp	Glu	Met	Asp	Leu	Glu	Pro	Asn		
			820					825					830				
Glu	Val	Arg	Leu	Glu	Gln	Gln	Ser	Val	Pro	Ala	Ala	Val	Phe	Gly	Ser		
		835					840					845					
Leu	Lys	Glu	Asp														
850																	

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Met	Phe	Ser	Ala	Leu	Lys	Lys	Leu	Val	Gly	Ser	Asp	Gln	Ala	Pro	Gly		
1				5					10					15			
Arg	Asp	Lys	Asn	Ile	Pro	Ala	Gly	Leu	Gln	Ser	Met	Asn	Gln	Ala	Leu		
			20					25					30				
Gln	Arg	Arg	Phe	Ala	Lys	Gly	Val	Gln	Tyr	Asn	Met	Lys	Ile	Val	Ile		
		35					40					45					
Arg	Gly	Asp	Arg	Asn	Thr	Gly	Lys	Thr	Ala	Leu	Trp	His	Arg	Leu	Gln		
	50					55					60						
Gly	Arg	Pro	Phe	Val	Glu	Glu	Tyr	Ile	Pro	Thr	Gln	Glu	Ile	Gln	Val		
65					70					75				80			
Thr	Ser	Ile	His	Trp	Ser	Tyr	Lys	Thr	Thr	Asp	Asp	Ile	Val	Lys	Val		
			85						90					95			
Glu	Val	Trp	Asp	Val	Val	Asp	Lys	Gly	Lys	Cys	Lys	Lys	Arg	Gly	Asp		
			100					105					110				
Gly	Leu	Lys	Met	Glu	Asn	Asp	Pro	Gln	Glu	Xaa	Glu	Ser	Glu	Met	Ala		
	115						120					125					
Leu	Asp	Ala	Glu	Phe	Leu	Asp	Val	Tyr	Lys	Asn	Cys	Asn	Gly	Val	Val		
130						135					140						
Met	Met	Phe	Asp	Ile	Thr	Lys	Gln	Trp	Thr	Phe	Asn	Tyr	Ile	Leu	Arg		
145					150					155				160			
Glu	Leu	Pro	Lys	Val	Pro	Thr	His	Val	Pro	Val	Cys	Val	Leu	Gly	Asn		
			165					170						175			
Tyr	Arg	Asp	Met	Gly	Glu	His	Arg	Val	Ile	Leu	Pro	Asp	Asp	Val	Arg		
		180						185					190				
Asp	Phe	Ile	Asp	Asn	Leu	Asp	Arg	Pro	Pro	Gly	Ser	Ser	Tyr	Phe	Arg		
	195						200					205					
Tyr	Ala	Glu	Ser	Ser	Met	Lys	Asn	Ser	Phe	Gly	Leu	Lys	Tyr	Leu	His		
210						215					220						
Lys	Phe	Phe	Asn	Ile	Pro	Phe	Leu	Gln	Leu	Gln	Arg	Glu	Thr	Leu	Leu		
225					230					235				240			
Arg	Gln	Leu	Glu	Thr	Asn	Gln	Leu	Asp	Met	Asp	Ala	Thr	Leu	Glu	Glu		
			245					250						255			
Leu	Ser	Val	Gln	Gln	Glu	Thr	Glu	Asp	Gln	Asn	Tyr	Gly	Ile	Phe	Leu		
		260					265						270				
Glu	Met	Met	Glu	Ala	Arg	Ser	Arg	Gly	His	Ala	Ser	Pro	Leu	Ala	Ala		
	275						280					285					
Asn	Gly	Gln	Ser	Pro	Ser	Pro	Gly	Ser	Gln	Ser	Pro	Val	Leu	Pro	Ala		
290						295					300						
Pro	Ala	Val	Ser	Thr	Gly	Ser	Ser	Ser	Pro	Gly	Thr	Pro	Gln	Pro	Ala		

305						310						315						320
Pro	Gln	Leu	Pro	Leu	Asn	Ala	Ala	Pro	Pro	Ser	Ser	Val	Pro	Pro	Val			
					325						330						335	
Pro	Pro	Ser	Glu	Ala	Leu	Pro	Pro	Pro	Ala	Cys	Pro	Ser	Ala	Pro	Ala			
					340						345						350	
Pro	Arg	Arg	Ser	Ile	Ile	Ser	Arg	Leu	Phe	Gly	Thr	Ser	Pro	Ala	Thr			
					355						360						365	
Glu	Ala	Ala	Pro	Pro	Pro	Pro	Glu	Pro	Val	Pro	Ala	Ala	Gln	Gly	Pro			
					370						375						380	
Ala	Thr	Val	Gln	Ser	Val	Glu	Asp	Phe	Val	Pro	Asp	Asp	Arg	Leu	Asp			
					385						390						400	
Arg	Ser	Phe	Leu	Glu	Asp	Thr	Thr	Pro	Ala	Arg	Asp	Glu	Lys	Lys	Val			
					405						410						415	
Gly	Ala	Lys	Ala	Ala	Gln	Gln	Asp	Ser	Asp	Ser	Asp	Gly	Glu	Ala	Leu			
					420						425						430	
Gly	Gly	Asn	Pro	Met	Val	Ala	Gly	Phe	Gln	Asp	Asp	Val	Asp	Leu	Glu			
					435						440						445	
Asp	Gln	Pro	Arg	Gly	Ser	Pro	Pro	Leu	Pro	Ala	Gly	Pro	Val	Pro	Ser			
					450						455						460	
Gln	Asp	Ile	Thr	Leu	Ser	Ser	Glu	Glu	Glu	Ala	Glu	Val	Ala	Ala	Pro			
					465						470						480	
Thr	Lys	Gly	Pro	Ala	Pro	Ala	Pro	Gln	Gln	Cys	Ser	Glu	Pro	Glu	Thr			
					485						490						495	
Lys	Trp	Ser	Ser	Ile	Pro	Ala	Ser	Lys	Pro	Arg	Arg	Gly	Thr	Ala	Pro			
					500						505						510	
Thr	Arg	Thr	Ala	Ala	Pro	Pro	Trp	Pro	Gly	Gly	Val	Ser	Val	Arg	Thr			
					515						520						525	
Gly	Pro	Glu	Lys	Arg	Ser	Ser	Thr	Arg	Pro	Pro	Ala	Glu	Met	Glu	Pro			
					530						535						540	
Gly	Lys	Gly	Glu	Gln	Ala	Ser	Ser	Ser	Glu	Ser	Asp	Pro	Glu	Gly	Pro			
					545						550						560	
Ile	Ala	Ala	Gln	Met	Leu	Ser	Phe	Val	Met	Asp	Asp	Pro	Asp	Phe	Glu			
					565						570						575	
Ser	Glu	Gly	Ser	Asp	Thr	Gln	Arg	Arg	Ala	Asp	Asp	Phe	Pro	Val	Arg			
					580						585						590	
Asp	Asp	Pro	Ser	Asp	Val	Thr	Asp	Glu	Asp	Glu	Gly	Pro	Ala	Glu	Pro			
					595						600						605	
Pro	Pro	Pro	Pro	Lys	Leu	Pro	Leu	Pro	Ala	Phe	Arg	Leu	Lys	Asn	Asp			
					610						615						620	
Ser	Asp	Leu	Phe	Gly	Leu	Gly	Leu	Glu	Glu	Ala	Gly	Pro	Lys	Glu	Ser			
					625						630						640	
Ser	Glu	Glu	Gly	Lys	Glu	Gly	Lys	Thr	Pro	Ser	Lys	Glu	Lys	Lys	Lys			
					645						650						655	
Lys	Thr	Lys	Ser	Phe	Ser	Arg	Val	Leu	Leu	Glu	Arg	Pro	Arg	Ala	His			
					660						665						670	
Arg	Phe	Ser	Thr	Arg	Val	Gly	Tyr	Gln	Val	Ser	Val	Pro	Asn	Ser	Pro			
					675						680						685	
Tyr	Ser	Glu	Ser	Tyr														
					690													